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Table 1E. BLAST results for NOV1a

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
ptnr:SPTREMBL- ACC:Q9D398	6330415E02RIK PROTEIN - Mus musculus (Mouse)	945	862/945 (91%)	897/945 (94%)	0.0
ptnr:SPTREMBL- ACC:O08722	TRANSMEMBRANE RECEPTOR UNC5H2	945	862/945 (91%)	893/945 (94%)	0.0
ptnr:SPTREMBL- ACC:O08747	UNC-5 HOMOLOG (C. ELEGANS)	931	610/929 (65%)	723/929 (77%)	0.0
ptnr:SPTREMBL- ACC:O95185	TRANSMEMBRANE RECEPTOR UNC5C - Homo sapiens	931	598/929 (64%)	718/929 (77%)	0.0

The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 1F. In the ClustalW alignment of the NOV1 proteins, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.

Table 1F. ClustalW Analysis of NOV1

10	1) NOV1a (SEQ ID NO:2) 2) NOV1b (SEQ ID NO:4) 3) ptnr: 6330415E02RIK PROTEIN - Mus musculus (Mouse) (SEQ ID NO:33) 4) ptnr: TRANSMEMBRANE RECEPTOR UNC5H2 (SEQ ID NO:34) 15 5) ptnr: UNC-5 HOMOLOG (C. ELEGANS) (SEQ ID NO:35) 6) ptnr: TRANSMEMBRANE RECEPTOR UNC5C - Homo sapiens (SEQ ID NO:36)	
20	NOV1a -----V CARSCA-RGALLLALLCWDPLRLSAGCTDSSE-----VLPDSFPSAPAEFLPFLPEPDAYIVVNKKPVE NOV1b -----V CARSCA-RGALLLALLCWDPLRLSAGCTDSSE-----VLPDSFPSAPAEFLPFLPEPDAYIVVNKKPVE Q9D398 -----V RARSCV-FSALLLALLLCWDPLRLSAGCTDSSE-----VLPDSFPSAPAEFLPFLPEPDAYIVVNKKPVE 008722 -----V RARSCA-RGALLLALLLCWDPLRLSAGCTDSSE-----ALPDSFPSAPASQPLPHFLPEPDAYIVVNKKPVE 008747 MRKGLRATAAPCCLGICYLLOMVLPALAISLSEGTSASQDDEPPHELPIFPSCCPFLPLPHFLPEPDAYIVVNKKPWN 095185 MRKGLRATAAPCCLGICYLLOMVLPALAISLSEGTSASQDDEPPHELPIFPSCCPFLPLPHFLPEPDAYIVVNKKPWN	66
25	NOV1a LFCRAFPATOYFKKGEWWSNDHVTOECLDEATGLRVREVOEVSRQOVEELFGLEDYWCQCVAWSAGTTKSRRAYV NOV1b LFCRAFPATOYFKKGEWWSNDHVTOECLDEATGLRVREVOEVSRQOVEELFGLEDYWCQCVAWSAGTTKSRRAYV Q9D398 LFCRAFPATOYFKKGEWWSNDHVTOECLDEATGLRVREVOEVSRQOVEELFGLEDYWCQCVAWSAGTTKSRRAYV 008722 LFCRAFPATOYFKKGEWWSNDHVTOECLDEATGLRVREVOEVSRQOVEELFGLEDYWCQCVAWSAGTTKSRRAYV 008747 LYCNASPATOYFKKGEWWSNDHVWDPRVDEPSGLIVREVSEIERSQOVEELFGEDYWCQCVAWSAGTTKSRRAYV 095185 LYCNASPATOYFKKGEWWSNDHVWDPRVDEPSGLIVREVSEIERSQOVEELFGEDYWCQCVAWSAGTTKSRRAYV	146
30	NOV1a RIAYLRRNFDQEPPLGKEVPLDHEVLLQCRPPEGVPVAEVWLRNEDVIDPQDTNFLTIDHLLIIQARLSDTANYTCAV NOV1b RIAYLRRNFDQEPPLGKEVPLDHEVLLQCRPPEGVPVAEVWLRNEDVIDPQDTNFLTIDHLLIIQARLSDTANYTCAV Q9D398 RIAYLRRNFDQEPPLGKEVPLDHEVLLQCRPPEGVPVAEVWLRNEDVIDPQDTNFLTIDHLLIIQARLSDTANYTCAV 008722 RIAYLRRNFDQEPPLGKEVPLDHEVLLQCRPPEGVPVAEVWLRNEDVIDPQDTNFLTIDHLLIIQARLSDTANYTCAV 008747 RIAYLRTKTFDQEPPLGKEVSLQEVLLQCRPPEGVPVAEVWLRNEDVIDPQDTNFLTIDHLLIIQARLSDTANYTCAV 095185 RIAYLRTKTFDQEPPLGKEVSLQEVLLQCRPPEGVPVAEVWLRNEDVIDPQDTNFLTIDHLLIIQARLSDTANYTCAV	226
35	NOV1a AKNIVAKRSTTATVIVVNGGWSWAESWPCSGRCGRGQOKRTRCTNPAPLNGGAFCEGQEQKTAATTCPVDCANT NOV1b AKNIVAKRSTTATVIVVNGGWSWAESWPCSGRCGRGQOKRTRCTNPAPLNGGAFCEGQEQKTAATTCPVDCANT Q9D398 AKNIVAKRSTTATVIVVNGGWSWAESWPCSGRCGRGQOKRTRCTNPAPLNGGAFCEGQEQKTAATTCPVDCANT 008722 AKNIVAKRSTTATVIVVNGGWSWAESWPCSGRCGRGQOKRTRCTNPAPLNGGAFCEGQEQKTAATTCPVDCANT 008747 AKNIVAKRSTTATVIVVNGGWSWAESWPCSGRCGRGQOKRTRCTNPAPLNGGAFCEGQEQKTAATTCPVDCANT 095185 AKNIVAKRSTTATVIVVNGGWSWAESWPCSGRCGRGQOKRTRCTNPAPLNGGAFCEGQEQKTAATTCPVDCANT	306
40	NOV1a EWSKWSACSTFCAHWSRBCMAPPPCGRDCSGTLDSHCTDGI.CMC-----LPSGDALYAGIVVATFV NOV1b EWSKWSACSTFCAHWSRBCMAPPPCGRDCSGTLDSHCTDGI.CMC-----LPSGDALYAGIVVATFV Q9D398 EWSKWSACSTFCAHWSRBCMAPPPCGRDCSGTLDSHCTDGI.CMC-----LPSGDALYAGIVVATFV 008722 EWSKWSACSTFCAHWSRBCMAPPPCGRDCSGTLDSHCTDGI.CMC-----LPSGDALYAGIVVATFV 008747 EWSKWSACSTFCAHWSRBCMAPPPCGRDCSGTLDSHCTDGI.CMC-----LPSGDALYAGIVVATFV 095185 EWSKWSACSTFCAHWSRBCMAPPPCGRDCSGTLDSHCTDGI.CMC-----LPSGDALYAGIVVATFV	374
45	Nov1a	

5	NOV1a Q9D398 008722 008747 095185	EWSKWSACSTECAHRSRECHAPPCGGRDCSGTLLDSNCTDGLCNC-----I.E.SGEAALYAGLVVAIFV EWSKWSACSTECAHRSRECHAPPCGGRDCSGTLLDSNCTDGLCIVLNORTLNDPKSHPLEISCDVALYAGLVVAVFV EWSKWSACSTECAHRSRECHAPPCGGRDCSGTLLDSNCTDGLCIVLNORTLNDPKSRPLEISGEVALYAGLVVAVFV SWSKWSACSTECATMFRRECIAFPAPXGGKOCGIVLQSNCTDGLCNC-----APSDVALYVAVVAVFV WWSKWSACSTECATMFRRECIAFPAPXGGKOCGIVLQSNCTDGLCNC-----APSDVALYVGLVIAAVFV	374 386 386 389 389			
10	NOV1a NOV1b Q9D398 008722 008747 095185	WAAILMAVCVIVYRRNCRDFDTIDDSAALTGGFPVNFKTPSPVQOLLHPSVPPDTASAGIYRCPPVYALODSADKI WAAILMAVCVIVYRRNCRDFDTIDDSAALTGGFPVNFKTPSPVQOLLHPSVPPDTASAGIYRCPPVYALODSADKI WAAILMAVCVIVYRRNCRDFDTIDDSAALTGGFPVNFKTPSPVQOLLHPSVPPDTASAGIYRCPPVYALODSADKI GLAIIWVAVVIVYRRNCRDFDTIDDSFAINGGFOPVNIAAF-CE-L-TAVPPDITAAWYRCPPVYALODSADKI GLAIIWVAVVIVYRRNCRDFDTIDDSFAINGGFOPVNIAAF-CE-L-TAVPPDITAAWYRCPPVYALODSADKI	454 454 466 466 463 463			
15	NOV1a NOV1b Q9D398 008722 008747 095185	PMTNSPLLDPLPLSLWIKVYSSSTIGSCGILADGADLLGVLPPIGTYPSPDFPRDTHFLHLRSASLGSO.LLGLPRDFESSVS PMTNSPLLDPLPLSLWIKVYSSSTIGSCGILADGADLLGVLPPIGTYPSPDFPRDTHFLHLRSASLGSO.LLGLPRDFESSVS PMTNSPLLDPLPLSLWIKVYSSSTIGSCGILADGADLLGVLPPIGTYPFCDFSRDTHFLHLRSASLGSO.LLGLPRDFESSVS PMTNSPLLDPLPLSLWIKVYSSSTIGSCGILADGADLLGVLPPIGTYPFCDFSRDTHFLHLRSASLGSO.LLGLPRDFESSVS PMTNSPLLDPLPLSLWIKVYSSSTIGSCGILADGADLLGVLPPIGTYPFCDFSRDTHFLHLRSASLGSO.LLGLPRDFESSVS	534 534 546 546 533 533			
20	NOV1a NOV1b Q9D398 008722 008747 095185	GTFGCLGGRILSIPCTGCVSLVNGAIPOCKFYEMVLIINN.FSTLPLSEGQTVLSPSVTCGPTGLLLCRPVILTHPHCA GTFGCLGGRILSIPCTGCVSLVNGAIPOCKFYEMVLIINN.FSTLPLSEGQTVLSPSVTCGPTGLLLCRPVILTHPHCA GTFGCLGGRILSIPCTGCVSLVNGAIPOCKFYEMVLIINN.FSTLPLSEGQTVLSPSVTCGPTGLLLCRPVILTHPHCA GTFGCLGGRILSIPCTGCVSLVNGAIPOCKFYEMVLIINN.FSTLPLSEGQTVLSPSVTCGPTGLLLCRPVILTHPHCA GTFGCLGGRILSIPCTGCVSLVNGAIPOCKFYEMVLIINN.FSTLPLSEGQTVLSPSVTCGPTGLLLCRPVILTHPHCA	614 614 626 626 613 613			
25	NOV1a NOV1b Q9D398 008722 008747 095185	EVSANDWIFOLKTQAHQGHWEEVVTLDEETLVTIPCYCOLEPRAACH:LLDOLCITYVFIGESYSRSAVKRLQLAVFAPALCT EVSANDWIFOLKTQAHQGHWEEVVTLDEETLVTIPCYCOLEPRAACH:LLDOLCITYVFIGESYSRSAVKRLQLAVFAPALCT EVIACCWIFOLKTQAHQGHWEEVVTLDEETLVTIPCYCOLEPRAACH:LLDOLCITYVFIGESYSRSAVKRLQLAVFAPALCT EVIAACCWIFOLKTQAHQGHWEEVVTLDEETLVTIPCYCOLEPRAACH:LLDOLCITYVFIGESYSRSAVKRLQLAVFAPALCT DTSIDEDWKLQLAQAOVOCMEWVWVCEENITTPCYIOLDAAEACHITENLSTHALVOSOHNAAKRKLAIFCPLOC DTSIDEDWKLQLAQAOVOCMEWVWVCEENITTPCYIOLDAAEACHITENLSTHALVOSOHNAAKRKLAIFCPLOC	694 694 706 706 693 693			
30	NOV1a NOV1b Q9D398 008722 008747 095185	SLEYSLRVYCLEDTPVALKEVLELERLTGGYLVEEPKFLFKDSDYHNLRLSLHDU.PHAHWRSKLLAKYQEIPFYHWSGS SLEYSLRVYCLEDTPVALKEVLELERLTGGYLVEEPKFLFKDSDYHNLRLSLHDU.PHAHWRSKLLAKYQEIPFYHWSGS SLEYSLRVYCLEDTPVALKEVLELERLTGGYLVEEPKFLFKDSDYHNLRLSLHDU.PHAHWRSKLLAKYQEIPFYHWSGS SLEYSLRVYCLEDTPVALKEVLELERLTGGYLVEEPKFLFKDSDYHNLRLSLHDU.PHAHWRSKLLAKYQEIPFYHWSGS SLEYSLRVYCLEDTPVALKEVLELERLTGGYLVEEPKFLFKDSDYHNLRLSLHDU.PHAHWRSKLLAKYQEIPFYHWSGS	774 774 786 786 773 773			
35	NOV1a NOV1b Q9D398 008722 008747 095185	QALHCTFTLERSLASTELTCMVVRQVEGEGQIFQLHTTIAETPAGSLD.LCSAPGSTVTTQLGPYAFKIPLSIRQK QALHCTFTLERSLASTELTCMVVRQVEGEGQIFQLHTTIAETPAGSLD.LCSAPGSTVTTQLGPYAFKIPLSIRQK QALHCTFTLERSLASTELTCMVVRQVEGEGQIFQLHTTIAETPAGSLD.LCSAPGSTVTTQLGPYAFKIPLSIRQK QALHCTFTLERSLASTELTCMVVRQVEGEGQIFQLHTTIAETPAGSLD.LCSAPGSTVTTQLGPYAFKIPLSIRQK QALHCTFTLERSLASTELTCMVVRQVEGEGQIFQLHTTIAETPAGSLD.LCSAPGSTVTTQLGPYAFKIPLSIRQK	854 854 866 866 852 852			
40	NOV1a NOV1b Q9D398 008722 008747 095185	QALHCTFTLERSLASTELTCMVVRQVEGEGQIFQLHTTIAETPAGSLD.LCSAPGSTVTTQLGPYAFKIPLSIRQK QALHCTFTLERSLASTELTCMVVRQVEGEGQIFQLHTTIAETPAGSLD.LCSAPGSTVTTQLGPYAFKIPLSIRQK QALHCTFTLERSLASTELTCMVVRQVEGEGQIFQLHTTIAETPAGSLD.LCSAPGSTVTTQLGPYAFKIPLSIRQK QALHCTFTLERSLASTELTCMVVRQVEGEGQIFQLHTTIAETPAGSLD.LCSAPGSTVTTQLGPYAFKIPLSIRQK QALHCTFTLERSLASTELTCMVVRQVEGEGQIFQLHTTIAETPAGSLD.LCSAPGSTVTTQLGPYAFKIPLSIRQK	933 933 945 945 931 931			
45	NOV1a NOV1b Q9D398 008722 008747 095185	CSSLDAPOJWRMLAQLMSDRYIINYFATKASPTGVILDWLWEAQODDGDLNLSASALEEMGKSEMLVAVATDGDC CSSLDAPOJWRMLAQLMSDRYIINYFATKASPTGVILDWLWEAQODDGDLNLSASALEEMGKSEMLVAVATDGDC CSSLDAPOJWRMLAQLMSDRYIINYFATKASPTGVILDWLWEAQODDGDLNLSASALEEMGKSEMLVAVATDGDC CSSLDAPOJWRMLAQLMSDRYIINYFATKASPTGVILDWLWEAQODDGDLNLSASALEEMGKSEMLVAVATDGDC CSSLDAPOJWRMLAQLMSDRYIINYFATKASPTGVILDWLWEAQODDGDLNLSASALEEMGKSEMLVAVATDGDC	933 933 945 945 931 931			
50	NOV1a NOV1b Q9D398 008722 008747 095185	CSSLDAPOJWRMLAQLMSDRYIINYFATKASPTGVILDWLWEAQODDGDLNLSASALEEMGKSEMLVAVATDGDC CSSLDAPOJWRMLAQLMSDRYIINYFATKASPTGVILDWLWEAQODDGDLNLSASALEEMGKSEMLVAVATDGDC CSSLDAPOJWRMLAQLMSDRYIINYFATKASPTGVILDWLWEAQODDGDLNLSASALEEMGKSEMLVAVATDGDC CSSLDAPOJWRMLAQLMSDRYIINYFATKASPTGVILDWLWEAQODDGDLNLSASALEEMGKSEMLVAVATDGDC CSSLDAPOJWRMLAQLMSDRYIINYFATKASPTGVILDWLWEAQODDGDLNLSASALEEMGKSEMLVAVATDGDC	933 933 945 945 931 931			
55						

The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (<http://www.ebi.ac.uk/interpro>). DOMAIN results for NOV1 as disclosed in Tables 1G-1O, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For Tables 1G-1O and all successive DOMAIN sequence alignments, fully conserved single residues are indicated by black shading or by the sign (!) and “strong” semi-conserved residues are indicated by grey shading or by the sign (+). The “strong” group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW.

Precursor (EC 3.1.3.48)) (E = 0.0). Public amino acid databases include the GenBank databases, SwissProt, PDB and PIR.

NOV2c is expressed in at least Synovium/Synovial membrane, Kidney. Expression information was derived from the tissue sources of the sequences that were included in the derivation of the sequence of CuraGen Acc. No. CG50718-05. The sequence is predicted to be expressed in the *Rattus norvegicus* :glomerular mesangial. because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:AF063249|acc:AF063249.1) a closely related *Rattus norvegicus* glomerular mesangial cell receptor protein-tyrosine phosphatase precursor (PTPRQ) mRNA, complete cds homolog.

Homologies among each of the above NOV2 proteins will be shared by the other NOV2 proteins insofar as they are homologous to each other as shown below in Table 2G. Any reference to NOV2 is assumed to refer to all three of the NOV2 proteins in general, unless otherwise noted.

15

Table 2G Alignment of NOV2a, b, and c

	10	20	30	40	50	60	
NOV2a	MDFLIIFLLLFIGTSETQVDVSNNVPGTRYDITISSISSTTYTSPVTRIGASN					EPGPPV	58
NOV2b	MDFLIIFLLLFIGTSETQVDVSNNVPGTRYDITISSISSTTYTSPVTRIGASN					EPGPPV	1
NOV2c	MDFLIIFLLLFIGTSETQVDVSNNVPGTRYDITISSISSTTYTSPVTRIGASN					EPGPPV	60
	70	80	90	100	110	120	
NOV2a	FLAGERVGSGAGILLSWNTPPNPNGRIISYIVKYKEVCPWMQTVYTQVRSKPD	SLEVLLTN					118
NOV2b	FLAGERVGSGAGILLSWNTPPNPNGRIISYIVKYKEVCPWMQTVYTQVRSKPD	SLEVLLTN					1
NOV2c	FLAGERVGSGAGILLSWNTPPNPNGRIISYIVKYKEVCPWMQTVYTQVRSKPD	SLEVLLTN					120
	130	140	150	160	170	180	
NOV2a	LNPGETTYEIKVAAENSAGIGVFSDPFLFOTAES	APGKVVDFTSEAVPFSS	-KLMWYTS-				175
NOV2b	LNPGETTYEIKVAAENSAGIGVFSDPFLFOTAES	APGKVVDFTSEAVPFSS	-KLMWYTS-				1
NOV2c	LNPGETTYEIKVAAENSAGIGVFSDPFLFOTAES	APGKVVDFTSEAVPFSS	-KLMWYTS-				180
	190	200	210	220	230	240	
NOV2a	ATKKKITSFKISVKHARSGIVVK	EVSIRVECILSASLPLHCNENSESFLWSTASPSPTLG					235
NOV2b	ATKKKITSFKISVKHARSGIVVK	EVSIRVECILSASLPLHCNENSESFLWSTASPSPTLG					1
NOV2c	ATKKKITSFKISVKHARSGIVVK	EVSIRVECILSASLPLHCNENSESFLWSTASPSPTLG					240
	250	260	270	280	290	300	
NOV2a	RVTPPSRTHSSSTLTONEISSV	KEPISFVVTHLRPYTTYLFEVSAATT	TEAGYIDSTIV				294
NOV2b	RVTPPSRTHSSSTLTONEISSV	KEPISFVVTHLRPYTTYLFEVSAATT	TEAGYIDSTIV				1
NOV2c	RVTPPSRTHSSSTLTONEISSV	KEPISFVVTHLRPYTTYLFEVSAATT	TEAGYIDSTIV				300
	310	320	330	340	350	360	
NOV2a	RTPESVPEGPPQNCTGNITGKFSILWDPP	TIVTGKFSYRVELYGP	-AGRILDNSTKDL				354
NOV2b	RTPESVPEGPPQNCTGNITGKFSILWDPP	TIVTGKFSYRVELYGP	-AGRILDNSTKDL				1
NOV2c	RTPESVPEGPPQNCTGNITGKFSILWDPP	TIVTGKFSYRVELYGP	-AGRILDNSTKDL				359
	370	380	390	400	410	420	
NOV2a	KFAFTNLTPFTMYDVYIAAET	SAGTGPKNISVFTPPDVGAVFDLOLAEVESTQVRITW					414

NOV2b ----- 1
 NOV2c KFAFTNLTPFTMYDVYIAAETSAGTGPKNISVFTPPDVPGAVFDLQLAEVESTOVRITW 419

5 430 440 450 460 470 480
 NOV2a KKPRQPNGIINQYRVKVLVPETGIILENTLLTGNNNEIDPMAPEIVNIVCPMVGLYEGSA 474
 NOV2b ----- 1
 NOV2c KKPRQPNGIINQYRVKVLVPETGIILENTLLTGNNNEIDPMAPEIVNIVCPMVGLYEGSA 479

10 490 500 510 520 530 540
 NOV2a EMSSDLHSLATFIYNSHPDKNFPARNRAEDQTSPVVTRNQYITDIAAEOLSYVIRLRR 534
 NOV2b ----- 1
 NOV2c EMSSDLHSLATFIYNSHPDKNFPARNRAEDQTSPVVTRNQYITDIAAEOLSYVIRLVP 539

15 550 560 570 580 590 600
 NOV2a EWAETMGSRSYTIMSSASRDNLSPG -PLSAQNPRVTHTVTHFVHWDPP -PVF 588
 NOV2b ----- 1
 NOV2c ETEHHMISVSAFTIMGEGPPTVLSVRTRQQVPSIININYKNISSSQULLIWDPPEYPNGK 599

20 610 620 630 640 650 660
 NOV2a FHHYLTITLDVENQSKSIHLRTLNSLTVLIGLKKYTKYKMRVAASTHVGESSLSEENDI 648
 NOV2b ----- 1
 NOV2c ITHYTAYAWEEDTNRAFCQTTIDNSFLTGIGLKKYTKYKMRVAASTHVGESSLSEENDI 659

25 670 680 690 700 710 720
 NOV2a FVRTSEDEPESSPQDVVEIDVTADEIRLKWSPEKPNGIIIAYEVLYKNIDTLYMKNTST 708
 NOV2b ----- 1
 NOV2c FVRTSEDEPESSPQDVVEIDVTADEIRLKWSPEKPNGIIIAYEVLYKNIDTLYMKNTST 719

30 730 740 750 760 770 780
 NOV2a TDIILRNLRPHTLYNISVRSYTRFGHGNQVSSLLSVRTSEAVPDSAPENITYKNISSGEI 768
 NOV2b ----- 1
 NOV2c TDIILRNLRPHTLYNISVRSYTRFGHGNQVSSLLSVRTSEAVPDSAPENITYKNISSGEI 779

35 790 800 810 820 830 840
 NOV2a ELSFLPPSSPONGIIQKYTIYLKRSGNGNEERTINTTSLTQNIKG LKKYTKYIIEVSASTLK 828
 NOV2b ----- 1
 NOV2c ELSFLPPSSPONGIIQKYTIYLKRSGNGNEERTINTTSLTQNI-LKKYTKYIIEVSASTLK 837

40 850 860 870 880 890 900
 NOV2a GEGVRAPSILTEEDAPDSPPQDFSVKQLSGVTVKLSWQPPLEPNQIILYYTVYVWF 886
 NOV2b ----- 1
 NOV2c GEGVRAPSILTEEDAPDSPPQDFSVKQLSGVTVKLSWQPPLEPNQIILYYTVYVWRNR 897

45 910 920 930 940 950 960
 NOV2a SSLKTINVTSLELSLDYDNVEYSAYVTASTRGDGKTRSNIISFQTPEGPSDPPKDVY 946
 NOV2b ----- 1
 NOV2c SSLKTINVTSLELSLDYDNVEYSAYVTASTRGDGKTRSNIISFQTPEGPSDPPKDVY 957

50 970 980 990 1000 1010 1020
 NOV2a YANLSSSSIILFWTPPSKPNQIIQYYSVYYRNNTSGTFMQNFTLHEVTNDFDNMVTSTIID 1006
 NOV2b ----- 1
 NOV2c YANLSSSSIILFWTPPSKPNQIIQYYSVYYRNNTSGTFMQNFTLHEVTNDFDNMVTSTIID 1017

55 1030 1040 1050 1060 1070 1080
 NOV2a KLTIFSYYTFWLTAUTSGVGNGNKSSDIIEVYTDQDVPEGFVGNLTYEISISSTAINVSWVP 1066
 NOV2b ----- 26
 NOV2c KLTIFSYYTFWLTAUTSGVGNGNKSSDIIEVYTDQDVPEGFVGNLTYEISISSTAINVSWVP 1077

60 1090 1100 1110 1120 1130 1140

NOV2a	PAQPNGLVYVYVSLILQQTPRHRVRPPLVTYERSIYFDNLEKYTDYLKITPSTEKGFSDT	1126
NOV2b	PAQPNGLVYVYVSLILQQTPRHRVRPPLVTYERSIYFDNLEKYTDYLKITPSTEKGFSDT	86
NOV2c	PAQPNGLVYVYVSLILQQTPRHRVRPPLVTYERSIYFDNLEKYTDYLKITPSTEKGFSDT	1137
	1150 1160 1170 1180 1190 1200	
NOV2a	YTAQLYIKTEEDVPETSPIINTFKNLSSSVLLSWDPPVKPNGAIISYDLYLQGPENENYS	1186
NOV2b	YTAQLYIKTEEDVPETSPIINTFKNLSSSVLLSWDPPVKPNGAIISYDLYLQGPENENYS	146
NOV2c	YTAQLYIKTEEDVPETSPIINTFKNLSSSVLLSWDPPVKPNGAIISYDLYLQGPENENYS	1197
	1210 1220 1230 1240 1250 1260	
NOV2a	FITSNDYIILEELSPFTLYSFAAARTRKGGLGPSSILFFYTDESVPLAPPQNLTLINCTS	1246
NOV2b	FITSNDYIILEELSPFTLYSFAAARTRKGGLGPSSILFFYTDESVPLAPPQNLTLINCTS	206
NOV2c	FITSNDYIILEELSPFTLYSFAAARTRKGGLGPSSILFFYTDESVPLAPPQNLTLINCTS	1257
	1270 1280 1290 1300 1310 1320	
NOV2a	DFVWLWKWSPSPSPPLGGIVKVYFSKIIHEHETDTIYYKNISGFKTEAKLVGLEPVSTYSIRVS	1306
NOV2b	DFVWLWKWSPSPSPPLGGIVKVYFSKIIHEHETDTIYYKNISGFKTEAKLVGLEPVSTYSIRVS	266
NOV2c	DFVWLWKWSPSPSPPLGGIVKVYFSKIIHEHETDTIYYKNISGFKTEAKLVGLEPVSTYSIRVS	1317
	1330 1340 1350 1360 1370 1380	
NOV2a	AFTKVGNGNQFSNVVKFTTQESVPDVVQNMQCMATSWQSVLVKWDPPKKANGIITQYMT	1366
NOV2b	AFTKVGNGNQFSNVVKFTTQESVPDVVQNMQCMATSWQSVLVKWDPPKKANGIITQYMT	326
NOV2c	AFTKVGNGNQFSNVVKFTTQESVPDVVQNMQCMATSWQSVLVKWDPPKKANGIITQYMT	1377
	1390 1400 1410 1420 1430 1440	
NOV2a	VERNSTKVSPQDHMYTFIKLLANTSYVFVKRASTSAGEGDESTCHVSTLPETVPSVPTNI	1426
NOV2b	VERNSTKVSPQDHMYTFIKLLANTSYVFVKRASTSAGEGDESTCHVSTLPETVPSVPTNI	386
NOV2c	VERNSTKVSPQDHMYTFIKLLANTSYVFVKRASTSAGEGDESTCHVSTLPETVPSVPTNI	1437
	1450 1460 1470 1480 1490 1500	
NOV2a	AFSDVQSTSATLTWIRPDITILGYFQNYKITTQLRAQKCKEWESEEECVEYQKIQYLYEAHL	1486
NOV2b	AFSDVQSTSATLTWIRPDITILGYFQNYKITTQLRAQKCKEWESEEECVEYQKIQYLYEAHL	446
NOV2c	AFSDVQSTSATLTWIRPDITILGYFQNYKITTQLRAQKCKEWESEEECVEYQKIQYLYEAHL	1497
	1510 1520 1530 1540 1550 1560	
NOV2a	TEETVYGLKKFRWYRFQVAASTNAGYGNASNWIISTKTLPGPPDGPPENVHVVATSPFSIS	1546
NOV2b	TEETVYGLKKFRWYRFQVAASTNAGYGNASNWIISTKTLPGPPDGPPENVHVVATSPFSIS	506
NOV2c	TEETVYGLKKFRWYRFQVAASTNAGYGNASNWIISTKTLPGPPDGPPENVHVVATSPFSIS	1557
	1570 1580 1590 1600 1610 1620	
NOV2a	ISWSEPAVITGPTCYLIDVKSVNDNFNISFIKSNEENKTIEIKDLEIFTRYSVVITAFT	1606
NOV2b	ISWSEPAVITGPTCYLIDVKSVNDNFNISFIKSNEENKTIEIKDLEIFTRYSVVITAFT	566
NOV2c	ISWSEPAVITGPTCYLIDVKSVNDNFNISFIKSNEENKTIEIKDLEIFTRYSVVITAFT	1617
	1630 1640 1650 1660 1670 1680	
NOV2a	GNISAAYVEGKSSAEMIVTTLESAPKDPPNNMTFQKIPDVEVTKFQLTSLPPSQPNGNIQV	1666
NOV2b	GNISAAYVEGKSSAEMIVTTLESAPKDPPNNMTFQKIPDVEVTKFQLTSLPPSQPNGNIQV	626
NOV2c	GNISAAYVEGKSSAEMIVTTLESAPKDPPNNMTFQKIPDVEVTKFQLTSLPPSQPNGNIQV	1677
	1690 1700 1710 1720 1730 1740	
NOV2a	YQALVYREDDPTAVQIHNLSI1QKTNTFVIAMLEGLKGHTYNISVYAVNSAGAGPKVPM	1726
NOV2b	YQALVYREDDPTAVQIHNLSI1QKTNTFVIAMLEGLKGHTYNISVYAVNSAGAGPKVPM	686
NOV2c	YQALVYREDDPTAVQIHNLSI1QKTNTFVIAMLEGLKGHTYNISVYAVNSAGAGPKVPM	1737
	1750 1760 1770 1780 1790 1800	
NOV2a	RITMDIKAPARPKTKPTPIYDATGKLVLVTSTTITIRMPICYYSDDHGP1KNVQVLVTETG	1786
NOV2b	RITMDIKAPARPKTKPTPIYDATGKLVLVTSTTITIRMPICYYSDDHGP1KNVQVLVTETG	746
NOV2c	RITMDIKAPARPKTKPTPIYDATGKLVLVTSTTITIRMPICYYSDDHGP1KNVQVLVTETG	1797

		1810	1820	1830	1840	1850	1860	
5	NOV2a	AQHDGNVTKWYDAYFNKARPYFTNEGFPNPPCTEGKTKFSGNEEYIYI	I	GADNACMIPGNE		1846		
	NOV2b	AOHDGNVTKWYDAYFNKARPYFTNEGFPNPPCTEGKTKFSGNEEYIYI	I	GADNACMIPGNE		806		
	NOV2c	AQHDGNVTKWYDAYFNKARPYFTNEGFPNPPCTEGKTKFSGNEEYIYI	I	GADNACMIPGNE		1857		
		1870	1880	1890	1900	1910	1920	
10	NOV2a	DKICNGPLKPKKQYLFKFRATNIMQFTDSDYSDPVKTLGEGLSERTEIILSVTLCILS				1906		
	NOV2b	DKICNGPLKPKKQYLFKFRATNIMQFTDSDYSDPVKTLGEGLSERTE-----				855		
	NOV2c	DKICNGPLKPKKQYLFKFRATNIMQFTDSDYSDPVKTLGEGLSERTEIILSVTLCILS				1917		
		1930	1940	1950	1960	1970	1980	
15	NOV2a	IILLGTIAIFAFARIROKQKEGGTYSPQDAEIIDTKLKDQLITVADLELKDERLTR				1962		
	NOV2b	-----				855		
	NOV2c	IILLGTIAIFAFARIROKQKEGGTYSPQDAEIIDTKLKDQLITVADLELKDERLTRLLSY				1977		
		1990	2000	2010	2020	2030	2040	
20	NOV2a	PISKKSFHQHVEELCTNNNLKFQEEFSelpkflodlsstdadlpwnraknfpni				2017		
	NOV2b	-----				855		
	NOV2c	RKSIXPISKKSFHQHVEELCTNNNLKFQEEFSelpkflodlsstdadlpwnraknfpni				2037		
		2050	2060	2070	2080	2090	2100	
25	NOV2a	KPYNNNRVKLIADASVPGSDYINASYISGYLCPNEFIATQGPLPGTVGDFWRMVWETRAK				2077		
	NOV2b	-----				855		
	NOV2c	KPYNNNRVKLIADASVPGSDYINASYISGYLCPNEFIATQGPLPGTVGDFWRMVWETRAK				2097		
		2110	2120	2130	2140	2150	2160	
35	NOV2a	TLVMLTQCFEKGRIRCHQYWPDENKPVTVFGDIVITKLMEDVQIDWTIRDLKIERHGDCM				2137		
	NOV2b	-----				855		
	NOV2c	TLVMLTQCFEKGRIRCHQYWPDENKPVTVFGDIVITKLMEDVQIDWTIRDLKIERHGDCM				2157		
		2170	2180	2190	2200	2210	2220	
40	NOV2a	TVRQCNFTAWPHEGVPENSAPLIHFVKLVRASRAHDTTPMIVHCSAGVGRITGVFIALDHL				2197		
	NOV2b	-----				855		
	NOV2c	TVRQCNFTAWPHEGVPENSAPLIHFVKLVRASRAHDTTPMIVHCSAGVGRITGVFIALDHL				2217		
		2230	2240	2250	2260	2270	2280	
45	NOV2a	TQHINDHDFVDIYGLVAELRSERMCMVONLAQYIFLHOCILDLLSNKGSNOPICFVNYS				2257		
	NOV2b	-----				855		
	NOV2c	TQHINDHDFVDIYGLVAELRSERMCMVONLAQYIFLHOCILDLLSNKGSNOPICFVNYS				2277		
		2290	2300					
50	NOV2a	LQKMDSDLAMEG-DVELEWEETTM	2281	(SEQ ID NO:6)				
	NOV2b	-----	855	(SEQ ID NO:8)				
	NOV2c	LQKMDSDLAMEG-DVELEWEETTM	2300	(SEQ ID NO:10)				
55								

The disclosed NOV2a polypeptide has homology to the amino acid sequences shown in the BLASTP data listed in Table 2H.

NOV2A -MDFLIIIFLLLFIGSETOVDVSNNVPGTRYDITISSIS--TTVTSPTM
gi|12621078| MMDFHFSPLPLIGTSESDMDVSSSFDCGTYDITLSSSVSA-TTVTSPTM
gi|125977| -----MGQOMTAARPEIAALSLVLSSLTWTWHPITIVDAAHPPPEIIRK
gi|10728878| -----MGQOMTAARPEIAALSLVLSSLTWTWHPITIVDAAHPPPEIIRK
5 gi|7290546| -MDCATRKQQQTRAHHQQQQIOQJOTHGRKRQQQOKQRHHHHYVONSOQQ
gi|1362625| -MDCATRKQQQTRAHHQQQQIOQJOTHGRKRQQQOKQRHHHHYVONPOQQ

60 70 80 90 100

10 NOV2A IGAS--NEPCCPVLAGERVGSAGILISWNTPPNPNGRIISWVVKYKEVC
gi|12621078| TLATNVTKPCPPVLAGERVGSAGILISWNTPPNPNGRIISWVVKYKEVC
gi|125977| PPNQGVRVGVGVASFYCAARGDPPPSIVWRKNGKKVSC-----
gi|10728878| PPNQGVRVGVGVASFYCAARGDPPPSIVWRKNGKKVSC-----
15 gi|7290546| OXHFVWLWVGLIHLIPLAOHANAADLVIT--IVENASSNANAFYRIDIYSPPF
gi|1362625| OXHFVWLWVGLIHLIPLARHANAADLVIT--IVENASSNANAFYRIDIYSPPF

110 120 130 140 150

20 NOV2A PPMOTVYVTKPDSLEVLTININPGTIIEIKVAAENSAGIGVFSDPFL
gi|12621078| PPMOTVYVTKPDSLEVLTININPGTIIEIKVAAENSAGIGVFSDPFL
gi|125977| -T-QSRYTIVLEQPGCGISILR1IEPVRACRDADPYECVAENGVGPAAVSADAT
gi|10728878| -T-QSRYTIVLEQPGCGISILR1IEPVRACRDADPYECVAENGVGPAAVSADAT
25 gi|7290546| GPPEPNTTIPASDIG-KDIKFSRALPGTEWFWIYYTNSTHREQLTWVN
gi|1362625| GPPEPNTTIPASDIC-KDIKFSRALPGTEWFWIYYTNSTHREQLTWVN

160 170 180 190 200

30 NOV2A FQTAESAPGKVVDFFGAEVPPSSK-LMWYTS-ATKIKITISEKISVKHNR
gi|12621078| FQTAESAPGKVVDLTLVEALNYSAVNLTINYLERQPNGKITSKISVKHARS
gi|125977| LTIYE-----GDKTIPAGFPVITCAGPGRTRVIEGHTVIMTCKAIG
gi|10728878| LTIYE-----GDKTIPAGFPVITCAGPGRTRVIEGHTVIMTCKAIG
35 gi|7290546| IITTAAPDPP--ANLSVOLRSSSKSAFTTWRPP--GSGRYSGERRVVLGLTD
gi|1362625| IITTAAPDPP--ANLSVOLRSSKSAAFTTWRPP--GSGRYSGERRVVLGLTD

210 220 230 240 250

40 NOV2A GIVVKEVISIRVECILSASLTLHCNENSESFLWSTASPSPTLGRVTPPSRT
gi|12621078| GIVVKDVSLRVEDILSGKLP--ECNENSESFLWSTASPSPTLGRVTPTVST
gi|125977| NTPPNIWKNOTKDMNSNPRYSLKDCFLQENSREEDQGKYECVAENSM
gi|10728878| NTPPNIWKNOTKDMNSNPRYSLKDCFLQENSREEDQGKYECVAENSM
45 gi|7290546| LPFERSYSLEGNETLQLSAK--ELTPCGSYQVOAYSVYQCKESVAYTSRN
gi|1362625| LPFERSYSLEGNETLQLSAK--ELTPCGSYQVOAYSVYQCKESVAYTSRN

260 270 280 290 300

50 NOV2A THESSSTLTQNEISSV-KEPISFVVTHLRPYTTYLFEVSAVTEACYIDST
gi|12621078| TOSSSSTAARKSISSVWKEPISFVVTHLRPYTTYLFEVSAVTEACYIDST
gi|125977| CTEHSKATNLVVKVRRVPPTFSRPPETISEVMIGSNLNLSCLIAVCGSPMPH
gi|10728878| CTEHSKATNLVVKVRRVPPTFSRPPETISEVMIGSNLNLSCLIAVCGSPMPH
55 gi|7290546| FTIUKPNTPGKELIVWFPRNEITLLVIVWOPPFAGIYTHYRVSITPDDAIOSV
gi|1362625| FTIUKPNTPGKELIVWFPRNEITLLVIVWOPPFAGIYTHYRVSITPDDAIOSV

310 320 330 340 350

60 NOV2A IIVRTPESVPGPPQNVCVTCMUTGKSFSTLWDPPPTIVTGKFSYRVELYGPS
gi|12621078| IIVRTPESVPGPPQNVCVTCMUTGKSFSTLWDPPPTIVTGKFSYRVELYGP
gi|125977| VKWMXKGSEDLTPENEMPICRNVL6LINTQESAN-----
gi|10728878| VKWMXKGSEDLTPENEMPICRNVL6LINTQESAN-----
65 gi|7290546| HYVERECEGEPGPQAQAFKCLAPGREYNISVQT-----
gi|1362625| HYVERECEGEPGPQAQAFKCLAPGREYNISVQT-----

360 370 380 390 400

70 NOV2A AGRILDNSTKDLKFAFTNLTPFTMYDVTIASTGAGTCKSNISVFTPPD
gi|12621078| SGRILDNSTKDLKFAFTNLTPFTMYDVTIASTGAGTCKSNISVFTPPD
gi|125977| -----YICIAASTLCOIDSVSVWKVGS-----
gi|10728878| -----YICIAASTLCOIDSVSVWKVGS-----
gi|7290546| VSEDEITS-SVPTIARYITVDEIR
gi|1362625| VSEDEITS-SVPTIARYITVDEIR

	410	420	430	440	450	
5	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	VEGAVFDFIOLAEVEESTOVRIIWKKPRQPNGLINQXRVRVLVPESTGIIMEN VEGAVFDFIOLAEVEESTOVRIIWKKPRQPNGLISQQRVKVSVDEIGVQIEN LPTAPTDVOISETVATSVRUEWSYKG-----PEDLOYYVIQYKPKAN LPTAPTDVOISETVATSVRUEWSYKG-----PEDLOYYVIQYKPKAN VLNVTFDEAYUTSSS-FRVRNPEPR-----TYSEFDAYQVMILSTSRRIFN VLNVTFDEAYUTSSS-FRVRNPEPR-----TYSEFDAYQVMILSTSRRIFN				
10		460	470	480	490	500
15	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	TLLTGNN-----INDPMAPEIIVNIVQFMVGLYEGSAEMSSDLHSLATFIYNSH TLLTGQD-----SISNPMSPEIMNLVDPMIG-----YEGSGEMSSDLHSPASFIYNSH QAFSEISG---IITMYVYRALSFYTEFYVIAVNNIGRG----- QAFSEISG---IITMYVYRALSFYTEFYVIAVNNIGRG----- VPRANG-----SVYFDYPDILEFGRTYEVVVVKTLADNVN----- VPRANG-----SVYFDYSPILEFGRTYEVVVVKTLADNVN-----				
20		510	520	530	540	550
25	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	PDKNEPARNAEDDTSPVJTRNQYITDIAAEQLTYVLIRLRRFWAETMG PHNDFPASTRAABEQSSPVVJTRNQYMTDITAQLSYVVRLLVPFTEHNTIS ----PPSAPATCTGETKMESAP----- ----PPSAPATCTGETEMESAP----- ---SWPASGEVILRPPVRSLG----- ---SWPASGEVILRPPVRSLG-----				
30	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	FSRYTIMSSASRDNLTSRG---PLSAQFRVTHVITIDEQFLHMWDPPDV VSAFTIMGEGPPTVLTVRTREQVPSSIQJUNYKNISSSSTLWYWDPPPEYP -----RNVQRTLSSSTTMVITWEPPETP----- -----RNVQRTLSSSTTMVITWEPPETP----- -----GFIDDR---SNAUHISWEPAAETG----- -----GFIDDR---SNAUHISWEPAAETG-----				
35		560	570	580	590	600
40	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	FFHHYLIFTLDVENOSKS---IILRTLNSLSLVIGKKTICKYKMRVAA NGKITHYDIYATELDINR---AFQMTTVDNSFLITCILKKYTRYKMRVAA NGQVTGYKYYTTNSNQPEASWNQMDVNSELTTVSDVTPHAITYTVRVOA NGQVTGYKYYTTNSNQPEASWNQMDVNSELTTVSELPHPAITYTVRVOA RQDSYRISYHEQTNASEV---PAPPVAAESEQITINLTEYTLDSLLAGR RQDSYRISYHEQTNASEV---PAPPVAAESEQITINLTEYTLDSLLAGR				
45		610	620	630	640	650
50	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	STHYGESLSSEENDIFVRTSEDEPESSPQDVEVIDVTADEIRLKWSPEK STHYGESLSSEENDIFVRTPEDEPESSPQDVQVTGVSPSELRLKWSPEK YTSMCAGPMSTP----- YTSMCAGPMSTP----- RYLDAVQALSKG----- RYLDAVQALSKG-----				
55		660	670	680	690	700
60	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	STHYGESLSSEENDIFVRTSEDEPESSPQDVEVIDVTADEIRLKWSPEK STHYGESLSSEENDIFVRTPEDEPESSPQDVQVTGVSPSELRLKWSPEK YTSMCAGPMSTP----- YTSMCAGPMSTP----- RYLDAVQALSKG----- RYLDAVQALSKG-----				
65		710	720	730	740	750
70	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546	PNGIIIAYEVLYKNIDLTYMKNTSTTDILRLRERPHLYNISVNSYTFG PNGIIIAYEVLYQNADTLFVKNTSTTDIIISDLKPKYLYNISIERSYTFG -----VOVKAQQGV----- -----VASNASDIT-----R-YTRP----- -----VASNASDIT-----R-YTRP-----				
		760	770	780	790	800
	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546	HGNQVSSLSSVRTSESVPDSAPENITYKNISSCEELISLPPSSENGILO HGNQSSSSLSSVRTSETVPDSAPENITYKNISSCEELISLPPRSPNGILO -----SQPSNFRATEIGETATIICQWIKPKPHSSENIV----- -----SQPSNFRATEIGETATIICQWIKPKPHSSENIV----- -----APLIQELASIDCG-----DMLSWRSVDNSRQD-----				

gi|1362625| -----AAPLIQELRSIDOG-----DMLSWRSVDNSRQD

	810	820	830	840	850
5	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	KYNTYIYKRSNG-NEERTINTISLTONIKGELKKYTOQIIIVYVSSTLAKGEGL KYTYIYKRSNS-HEARTINTISLTONIKGELKKYTHYVIEVSASILKGEGL HYELYWNDIYANCAHHKRISNSEAYTIDGLYEDTLYYIWLARSQRGEGLA HYELYWNDIYANCAHHKRISNSEAYTIDGLYEDTLYYIWLARSQRGEGLA RYEVYHQRGT-REERTMTATNETSLTIHYLHFGSGYEVKVAISH---GV RYEVYHQRGT-REERTMTATNETSLTIHYLHFGSGYEVKVAISH---GV			
10					
15	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	860 870 880 890 900 RSAPISTMTEEDAPDSSPPDFPSVKQLSGVTVKLSWOPP--LENGIILYY RSRPISNLTEDAPDSSPPDFPSVKQLSGVTVMLSWOPP--LENGIILYY TUPPIPMRKOWVPGAPPRTITAIATSSTTISLSWLPPPVERSNGRILYY TUPPIPMRKOWVPGAPPRTITAIATSSTTISLSWLPPPVERSNGRILYY RSEPHSYFQAVEP--KPPQNLTLQVHINLVVLLHWOAP--EGSD-FSEYV RSEPHSYFQAVEP--KPPQNLTLQVHINLVVLLHWOAP--EGSD-FSEYV			
20					
25	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	910 920 930 940 950 TIVVVWR---SSLXTIN-WTETSMELSDLDYVNEYSAVVTASTRFGDGKT TIVVVWDK---SSLRAIN-ATEASIVLSDLDYVNDYGACVTASTRFGDGNA KVFVVEVGREDDEATTMILNMISIVLDEEKRWTLEYKIVVLAGTSVGDC-P KVFVVEVGREDDEATTMILNMISIVLDEEKRWTLEYKIVVLAGTSVGDC-P VRYRTDA---SPWQRISSGULHNEARIKDMDHYGERYLVQVNNTVS-FGVESP VRYRTDA---SPWQRISSGULHNEARIKDMDHYGERYLVQVNNTVS-FGVESP			
30					
35	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	960 970 980 990 1000 RSNIISFOTPEG-PSDPPKDQVYANLSSSSIIIFWTPPPS-KPNGLIOYY RSSIINFRTPEGEPEPSDPNDVHYVNLSSSSIIFWTPPPV-KPNGLIOYY RSHPIIIRTCEDVPGD-PODVKATPLNSIISIVWSWKPPLEKDRNGIIRGY RSHPIIIRTCEDVPGD-PODVKATPLNSIISIVWSWKPPLEKDRNGIIRGY HPLELNITMPPQ---PVSNNVPLVDSRNLTLEKP---RFDCHVDFY HPLELNITMPPQ---PVSNNVPLVDSRNLTLEWP---RFDCHVDFY			
40	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	1010 1020 1030 1040 1050 SVYYRNTSGTFMQNFTLHEVTNDFDNMTVSTIIDKLTIFSYYTFWLTA SVYYQNTSGTFVQNFLLQVTKESDNVTVSARIYRLAIFSYYTFWLTA			
45					
50	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	1060 1070 1080 1090 1100 SVGNGNKSSDIIIEVYTDQDVPEGFVGVLNTYESISSTAINNSWVPPAOPNG SVGNGNKSSDIIHVYTDQDIPEGFVGVLNTFESISSTAIHNSWEPPSOPNG -----HIHAQELRDEC -----HIHAQELRDEG -----T-----IKWPTDREDR -----T-----OKWPTDSEDR			
55					
60	NOV2A gi 12621078 gi 125977 gi 10728878 gi 7290546 gi 1362625	1110 1120 1130 1140 1150 IVFYIVSILQOQP-RHVRPPLVTVYERSIVYDNLKEYIDMILKMTPTSER IVFYIVSILQOQP-RHVRPPLVTVYERSIVYDNLKEYIDMILKMTPTSER KGFLNEPFKEDWD-----TIEFNVTGLOPDITKNSIOVAALTRK KGFLNEPFKEDWD-----TIEFNVTGLOPDITKNSIOVAALTRK VEFKNVIQLEDLSS----P-SVRLPEDIISPGROWRFEVQASSN- VEFKNVIQLEDLSS----P-SVRLPEDIISPGROWRFEVQASSN-			
65					
70	NOV2A gi 12621078 gi 125977	1160 1170 1180 1190 1200 GFSPTYTAQIVIKIEEDIPETSPINTFNLSSSTSVLSSMPVVPNCAI GFSPTYTAQIVIKIEEDIPETSPINTFNLSSSTSVLSSMPVVPNCAI GDGERSAAIIVKTPGGVPVRPTVSKIMEREPIVSHLPWEPRACTYCEI			

gi 10728878	GDGDRSAAIWVKTPGGPVVRPTVS	KIMREPIV	SIDPEWERPAPTYCEI			
gi 7290546	G-----	IRSG	T-----			
gi 1362625	G-----	IRSG	T-----			
5	1210 1220 1230 1240 1250					
NOV2A	ISYDLTL---	OGPNENYSFITSNDV	WILSELSPTLIVSFFAAARTRKGQ			
gi 12621078	LGYHHTL-----	QGPANHTFVTSGNHTV	WILSELSPTLIVSFFAAARTMAGQ			
gi 125977	RGYRLRWGVKDQALKEEMLSGPQM	KKRFDNLERGVEN	YERVAGSNHIGI			
10	gi 10728878	RGYRLRWGVKDQALKEEMLSGPQM	KKRFDNLERGVEN	YERVAGSNHIGI		
gi 7290546	-----	DHISTRTMPLIQSVD	FIANAGHECQ			
gi 1362625	-----	DHISTRTMPLIQSVD	FIANAGHECQ			
15	1260 1270 1280 1290 1300					
NOV2A	GPSSILFLFYIDESVPLAPPONLTIN	CSDFWNLKNSPSPLPGGIVKV	IS			
gi 12621078	GPSSILFLFYIDESVPLAPPONLTIN	YNSDFWNLWSDSPSPLPGGIVKV	IS			
gi 125977	QEETVKIKIOTPEGTPGGPASNIT	TRFCQIPDVICVWDPPTREHRNGI	ITR			
gi 10728878	QEETVKIKIOTPEGTPGGPASNIT	TRFCQIPDVICVWDPPTREHRNGI	ITR			
20	gi 7290546	-----	DTHITLTSYTEDADSTRFD	IYR		
gi 1362625	-----	DTHITLTSYTEDADSTRFD	IYR			
25	1310 1320 1330 1340 1350					
NOV2A	FKKHHEHETDTIYYKNISGF	KTEAKLVGLEP	VSTYSIRVSAFTKVGNGNQP			
gi 12621078	FKKHHEHETDTVFYKNISGLQT	DAKLEGLEP	VSTYSVSVAFTKVGNGNQY			
gi 125977	MDVQFH-----	-----	-----			
gi 10728878	MDVQFH-----	-----	-----			
30	gi 7290546	FSMGD-----	-----			
gi 1362625	FSMGD-----	-----	-----			
35	1360 1370 1380 1390 1400					
NOV2A	SNVVKFITQESVPDVVQNMOCMATS	WQSVLVKWDDPKKANGIITQYMV	TV			
gi 12621078	SNVVVFITQESVPEAVRNIECVARD	WQSVSVRWDDPRKTNGIIHHYMI	IV			
gi 125977	-----	-----	KK-----	ID		
gi 10728878	-----	-----	KK-----	ID		
40	gi 7290546	-----	P-----	T1		
gi 1362625	-----	P-----	T1			
45	1410 1420 1430 1440 1450					
NOV2A	ERNSITIVSPDHMYLFIKLLANTSY	VEKVRASTSAGECDESTCHV	STIPE			
gi 12621078	GGNSITKVSPDPTYTFIKLLPNTS	YVVEVRASTSAGECNESRCDI	STIPE			
gi 125977	HGLGSEERNMLRKAVENILEEN	TEITLFRVRAYTKOACPFSDKL	IIVETER			
gi 10728878	HGLGSEERNMLRKAVENILEEN	TEITLFRVRAYTKOACPFSDKL	IIVETER			
gi 7290546	KDKEKLANDTERKLSPSCLTPGKLY	NVTWTVS-----	CGVASLPVQRLYR			
gi 1362625	KDKEKLANDTERKLSPSCLTPGKLY	NVTWTVS-----	CGVASLPVQRLYR			
50	1460 1470 1480 1490 1500					
NOV2A	TVPSVPNTIAFSDVQTSATL	TWIREDTILGYFONYKLT	TQLRAOKCKEW			
gi 12621078	TVPSAPTNIAFSNVQTSATL	WTWIKEDTIFGYFONYKLT	TQLRAOKCREW			
gi 125977	DMGRAPSMSQAEATSGTAEW	WIEPVTISRGKLLGYWIPY	TMTAVE-----			
55	gi 10728878	DMGRAPSMSQAEATSGTAEW	WIEPVTISRGKLLGYWIPY	TMTAVE-----		
gi 7290546	LHPLPISDIKAIQVAREITLH	WTAAGEYTD	FEIOLCYLSADEEAP-----			
gi 1362625	LHPLPISDIKAIQVAREITLH	WTAAGEYTD	FEIOLCYLSADEEAP-----			
60	1510 1520 1530 1540 1550					
NOV2A	ESEECVBYORIOYDYEAAHLTE	ETVGLKKFRWYRECOVAASINA	CGVNASN			
gi 12621078	EPEECISHQXDCYLYEANQTE	ETVHGLKKFRWYRECOVAASIN	VGYSNASE			
gi 125977	-----	-----	-----			
gi 10728878	-----	-----	-----			
65	gi 7290546	-----	-----	-----		
gi 1362625	CILQDN-----	MTKNT-----	TEITLQGLRPYHNWYTF	TVVVRSGS	EQG-----	
70	NOV2A	CILQDN-----	MTKNT-----	TEITLQGLRPYHNWYTF	TVVVRSGS	EQG-----
	1560 1570 1580 1590 1600					
	WESXTLPGPPEGPENHV	ATSPFSISWSWSPPAV	ITGPTC	LDVKS		

gi|12621078| gi|125977| gi|10728878| gi|7290546| gi|1362625| WISTOTLPGEPPDGPPENVHVATSPFGINISWSEPAVITGTFYLIIDVKS
KVIVRIK---PFDVPLNIRAHDVSTHSMTLSWSPIRLT-PVNYKISFDP
KVIVRIK---PFDVPLNIRAHDVSTHSMTLSWSPIRLT-PVNYKISFDP
-----TEFADSVSTIIMRSAPISASYQTLTAPPCKVLYFQPSD-
-----TEFADSVSTIIMRSAPISASYQTLTAPPCKVLYFQPSD-

1610 1620 1630 1640 1650

10 NOV2A
gi|12621078| gi|125977| gi|10728878| gi|7290546| gi|1362625| VDNDEFNISPIKSNEENKTIEIKDEIFTRYSVVITAFTGNISAAYVEGK
VDDDFNISFLKSNEENKTTEINNLLEVFTRYSVVITAFTGVGNVRAYTDGK
MK-
MK-
VQ-
VQ-

1660 1670 1680 1690 1700

15 NOV2A
gi|12621078| gi|125977| gi|10728878| gi|7290546| gi|1362625| SSAEMIVTTLESAPKDPNPNMIFOKIPDEVTKFQLTFPPSQPNCTQVY
SSAEVIITLLESAPKDPNPNMIFOKIPDEVTKFQLTFPPSQPNCTQVY
-----VFVDSOGHSQT-----QIVPKREIILKH
-----VFVDSOGFSQT-----QIVPKREIILKH
-----PGEVTFEWS-----LEPAEQHGPIDYE
-----PGEVTFEWS-----LEPAEQHGPIDYE

1710 1720 1730 1740 1750

20 NOV2A
gi|12621078| gi|125977| gi|10728878| gi|7290546| gi|1362625| QALVREDDPAVQIHNLSTIQKTNFTVIAMLEGALKGCCATYNISVYAVNS
QALVREDDPAVQIHNLSTIQKTNFTVIAMLEGALKGCCATYNISVYAVNS
YMKTHTINELSPFTTYNVNVAIPS-----DYSYRPPTKITVITQMAAQ
YMKTHTINELSPFTTYNVNVAIPS-----DYSYRPPTKITVITQMAAQ
RITCQNADDADVSSYEFPPNATQG-----KIDGLVPGNHYIFRLOAKSA
RITCQNADDADVSSYEFPPNATQG-----KIDGLVPGNHYIFRLOAKSA

1760 1770 1780 1790 1800

25 NOV2A
gi|12621078| gi|125977| gi|10728878| gi|7290546| gi|1362625| ACAGPKVPMRITMDIKAPARPKTPKTPIDYDATGKLLVTSTTITIRMPICY
ACAGPKVPMRITMDIKAPARPKSKPPIPDRATGKLLVTSTTITIRMPICY
PMVKPDYFGVNVNGEEILVILPOASEEYGPISH-----YYLWVVPEDKSN
PMVKPDYFGVNVNGEEILVILPOASEEYGPISH-----YYLWVVPEDKSN
LGYGAEREHIQTMPTILAPPVPEPSVTPIDEVSR-----TSSTIEISFRGCV
LGYGAEREHIQTMPTILAPPVPEPSVTPIDEVSR-----TSSTIEISFRGCV

1810 1820 1830 1840 1850

30 NOV2A
gi|12621078| gi|125977| gi|10728878| gi|7290546| gi|1362625| YSDDHCPKIVNVQVLVITGACHDG--NVTWKYDAVENKAR-PYFTNECEP
YNDDHCPKIVNVQVLVITGACHDG--NVTWKYDAVENKAR-PYFTNECEP
LHKIPDQFLIDDLIPGRNKPERPN----APYIAAKGPORSTIPETFHLCSG
LHKIPDQFLIDDLIPGRNKPERPN----APYIAAKGPORSIPETFHLCSG
FSNAHCMSYTYLTAEVGKAGASGLEEPSWODVQAYTVWLPHYQAIEPYN
FSNAHCMSYTYLTAEVGKAGASGLEEPSWODVQAYTVWLPHYQAIEPYN

1860 1870 1880 1890 1900

35 NOV2A
gi|12621078| gi|125977| gi|10728878| gi|7290546| gi|1362625| NPPCTECKTKFSGNEEIVYLIGADNACMIPGNEKDICKCNGPLKPKKQMLFKF
NPPCTECKTKFSGNEEIVYLIGADNACMIPGNEEKICNGPLKPKKQMLFKF
DDYHFTNRKLEREKRMHIFVRAVVDTPCKH--LYTSSPFSEFSLDMRE
DDYHFTNRKLEREKRMHIFVRAVVDTPCKH--LYTSSPFSEFSLDMRE
PFLTSNGSRKSSLABEFTIGTANCKHQAG--YCNGPLRAGTIVRIKI
PFLTSNGSRKSSLABEFTIGTANCKHQAG--YCNGPLRAGTIVRIKI

1910 1920 1930 1940 1950

40 NOV2A
gi|12621078| gi|125977| gi|10728878| gi|7290546| gi|1362625| RATNIMCGFTDSDYSDPVTLGEGLSERIVETIHSVTLCELNSIEHGTAI
RATNVMGCFTDSEYSIDPLKTLGEGLSERIVETIHSVTLCELNSIEHGTAI
APPGERPHRPDPNIPPEPVSVNRNKEPEIIEWVWVPLMUSIFESTALLI
APPGERPHRPDPNIPPEPVSVNRNKEPEIIEWVWVPLMUSIFESTALLI
RAFTBEDKFTDIDVYSSPITE-----R-SDTVIVATVSAVLAJAVLVW
RAFTBEDKFTDIDVYSSPITE-----R-SDTVIVATVSAVLAJAVLVW

1960 1970 1980 1990 2000

NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

5 FAFARIROK-----KEGGTYSPODABSIIDTKLKLDQIYVADLELKD
FAFVRIROK-----KEGGTYSPRDAEIIDDTKFKLDDLIIVADLELKD
VLCVVKRRLRPPCKTPDAAVTRPLMAADDGAGPTPSDPDMRRLNFTPG
VLCVVKRRLRPPCKTPDAAVTRPLMAADDGAGPTPSDPDMRRLNFTPG
VYCQHRCOLI-----RAASKLAR-----MODELAAPIPEGYHTPN-
VYCQHRCOLI-----RAASKLAR-----MODELAAPIPEGYHTPN-

10 NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

15 2010 2020 2030 2040 2050
WT-----RPISKKSPFLCHVEELCINNNIKFQEEFSLELPKFQFLQDLSS
STRLLSYRKSIKPKISKSPFLCHVEELCINNNIKFQEEFSLELPKFQFLQDLSS
MIS-----HEPIPSEEFANHHIERLKSNDNOKFSQEVESTEPG-QQFIW
MIS-----HEPIPSEEFANHHIERLKSNDNOKFSQEVESLEPG-QQFIW
-----RPVHVKDESEHYRIMSAADSDFRSEEEFEELKHVGRDQAC
-----RPVHVKDESEHYRIMSAADSDFRSEEEFEELKHVGRDQAC

20 2060 2070 2080 2090 2100
NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

25 ITADALPWNRAKNRFPNIKPYNNNRVKLIADASVPGSDYINAASYISGYLCP
ITADALPWNRAKNRFPNIKPYNNNRVKLIADVS3PGSDYINAASYISGYLCP
DNSNLEHNKSKNRYANNTAYDHRSVQLPAVEGVGSDYINANYCDGYRKH
DNSNLEHNKSKNRYANNTAYDHRSVQLPAVEGVGSDYINANYCDGYRKH
SEANLPONRPKNRFTINILPYDHSRFKLQPVDDDGSDYINANYMPGHNSP
SEANLPONRPKNRFTINILPYDHSRFKLQPVDDDGSDYINANYMPGHNSP

30 2110 2120 2130 2140 2150
NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

35 NEFIATQGPLPGTVGDFWRMVMETRAKTVMLTOCFEKGRIRHQYWPED
NEFIATQGPLPGTVGDFWRMVMETRAKTVMLTOCFEKGRIRHQYWPED
MAYVATQGPLQETFVDFWRMCWEILKATIVMTRLEERTRIKCDQYWPTR
MAYVATQGPLQETFVDFWRMCWEILKATIVMTRLEERTRIKCDQYWPTR
REFIVTQGPLHSTREEFWRCWEISNSRAIVMLTRCFEKGRKCDQYWPVD
REFIVTQGPLHSTREEFWRCWEISNSRAIVMLTRCFEKGRKCDQYWPVD

40 2160 2170 2180 2190 2200
NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

45 2210 2220 2230 2240 2250
NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

50 2260 2270 2280 2290 2300
NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

55 2310 2320 2330 2340 2350
NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

60 2310 2320 2330 2340 2350
NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

65 2310 2320 2330 2340 2350
NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

70 2310 2320 2330 2340 2350
NOV2A
gi|12621078|
gi|125977|
gi|10728878|
gi|7290546|
gi|1362625|

Tables 2J-2EE list the domain descriptions from DOMAIN analysis results against NOV2a. This indicates that the NOV2a sequence has properties similar to those of other proteins known to contain this domain.

50

Table 2J. Domain Analysis of NOV2a

gnl|Smart|smart00194, PTPc, Protein tyrosine phosphatase, catalytic domain (SEQ ID NO:93)
CD-Length = 264 residues, 99.6% aligned
Score = 318 bits (816), Expect = 2e-87

NOV 1: 1983 KFQEEFSLEPK-FLQDLSSTADLWPWNRAKNRFPNIKPYNNNRVKLIADASVPGSDYINA 2041
+ | | + | + | | | | | | | | + ++ | | ++ | | | | | | | | | | | |
Sbjct: 1 GLEEEFEKLQLRQLTPDDLSCVAILPENRDKNRYKDVLPYDHTRVKL-KPPPGEGSODYINA 59
NOV 1: 2042 SYISGGLCPNEFIATQGPLPGTVGDFWRMVWETRAKTLVMLTOCFEKGRIRCHOYWPEDN 2101

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 3D.

Table 3D. ClustalW Analysis of NOV3

5 1) NOV3 (SEQ ID NO:12)
6 2) ref|XP_027243.1| (XM_027243) hypothetical protein XP_027243 [Homo sapiens] (SEQ
7 ID NO:42)
8 3) gi|15076843|gb|AAK82958.1|AF233450_1 (AF233450) pecanex-like protein 1 [Homo
9 sapiens] (SEQ ID NO:43)
10 4) gi|6650377|gb|AAF21809.1|AF096286_1 (AF096286) pecanex 1 [Mus musculus] (SEQ
11 ID NO:44)
12 5) gi|13171105|gb|AAK13590.1|AF154413_1 (AF154413) pecanex [Takifugu rubripes] (SEQ
13 ID NO:45)
14 6) gi|7290294|gb|AAF45755.1| (AE003423) pcx gene product [alt 1] [Drosophila
15 melanogaster] (SEQ ID NO:46)

gi|15076843|gb| DFPLYQQRRGLDPVSELESSKPLSGSKESLVENSGLSGEFQLAGDLKINTSQPPTKSGKS 359
 gi|6650377|gb|A ----- 1
 gi|13171105|gb| ----- 151
 gi|7290294|gb|A ----- 1

5 370 380 390 400 410 420

NOV3
 ref|XP_027243.1 ----- 1
 gi|15076843|gb| KPLKAEKSMDSLRSLSTRSSGSTESYCSGTDRTNSTVSSYKSEQTSSTHIESILSEHEE 419
 gi|6650377|gb|A ----- 1
 gi|13171105|gb| ----- MDL 154
 gi|7290294|gb|A ----- 1

15 430 440 450 460 470 480

NOV3
 ref|XP_027243.1 ----- 1
 gi|15076843|gb| SPKAGTKSGRKKECCAGPEEKNSCASDKRTSSEKIAMEASTNSGVHEAKDPTPSDEMHNQ 479
 gi|6650377|gb|A ----- 1
 gi|13171105|gb| ----- 172
 gi|7290294|gb|A ----- 1

25 490 500 510 520 530 540

NOV3
 ref|XP_027243.1 ----- 1
 gi|15076843|gb| RGLSTSASEEANKPHANEFTSQGDRPPGNTAENKEEKSDFKSAVSVDSKVRKDVGKKQKE 539
 gi|6650377|gb|A ----- 1
 gi|13171105|gb| ----- 172
 gi|7290294|gb|A ----- 1

35 550 560 570 580 590 600

NOV3
 ref|XP_027243.1 ----- 1
 gi|15076843|gb| GDVRPKSSSVIHTASAHKGRRRTGKKRASSFDSSRHRDYVCFRGVSGTKPHSAIFCHD 599
 gi|6650377|gb|A ----- 1
 gi|13171105|gb| ----- S- 173
 gi|7290294|gb|A ----- 1

45 610 620 630 640 650 660

NOV3
 ref|XP_027243.1 ----- 1
 gi|15076843|gb| EDSSDQSDLRSASSVQSAHQFSSEDSSSTTSHSCQSPEGRYSALKTHKERGTDSEHT 659
 gi|6650377|gb|A ----- 1
 gi|13171105|gb| ----- 173
 gi|7290294|gb|A ----- 1

50 670 680 690 700 710 720

NOV3
 ref|XP_027243.1 ----- 1
 gi|15076843|gb| HKAHLVPEGTSKKRATRRSTSNTSAKTRARVLSDLSGTVACLNDSNRLMAPESIKPLTTS 719
 gi|6650377|gb|A ----- 1
 gi|13171105|gb| ----- 173
 gi|7290294|gb|A ----- 1

60 730 740 750 760 770 780

NOV3
 ref|XP_027243.1 ----- 1
 gi|15076843|gb| KSDLEAKEGEVLDLSSLGRASQLETVTRSRSNLPNVAFPEGEEQDAVSGAAQASEAV 779
 gi|6650377|gb|A ----- 1
 gi|13171105|gb| ----- EETV 177
 gi|7290294|gb|A ----- 1

70 790 800 810 820 830 840

NOV3 ref|XP_027243.1 1
 gi|15076843|gb| 1
 gi|6650377|gb|A 1
 gi|13171105|gb| 1
 gi|7290294|gb|A 1

5 SFRRERSTPQQAVRRRHAGSNPTPPPTLIGSPLSLQDGQQGQQSTAQ-----VKVQS 833
 IFRRERSTPQQAVRRRHAGSNPTPPTSIGSPLRYALHEADRPSGVRSWYRTVKSQPS 237
 ----- 1

850 860 870 880 890 900
 NOV3 ref|XP_027243.1 3
 gi|15076843|gb| 1
 gi|6650377|gb|A 3
 gi|13171105|gb| 1
 gi|7290294|gb|A 1

RPPSQAAVLSASASALLVRNGSVHLEASHDNASAVGGSSLHDELGKFSSTLYETGGCD 893
 RTPSQVTVLSTSASLLARNGSTHLEGSQDKASTVGTTSLQDEFGTLTTPSLEYIRGCH 297
 ----- 1

910 920 930 940 950 960
 NOV3 ref|XP_027243.1 57
 gi|15076843|gb| 1
 gi|6650377|gb|A 952
 gi|13171105|gb| 57
 gi|7290294|gb|A 356
 ----- 1

VNFEPAARRASN-IWDTDSHVSSSTSVRFYPHDVI-----RLNRLLTIDTDLLEQQDIDL 57
 VNFEPAARRASN-ICDTDSHVSSSTSVRFYPHDVI-SLPQIRLNRLLTIDTDLLEQQDIDL 952
 VNFEPAARRASN-ICDTDSHVSSSTSVRFYPHDVI-----LNRLLTIDTDLLEQQDIDL 57
 GNFESAPARRASNNIWDTDSHISSTSVRFYPHDVI-SLHHIRANRLLTIDPALLEQQDIDL 356
 ----- 1

970 980 990 1000 1010 1020
 NOV3 ref|XP_027243.1 112
 gi|15076843|gb| 1
 gi|6650377|gb|A 1007
 gi|13171105|gb| 112
 gi|7290294|gb|A 416
 ----- 1

SPDLAAT-----YGPTEAAQKVIGHYYREWILPQLWIGINFDRLTLLALFDRNREILEMV 112
 SPDLAAT-----YGPTEAAQKVIGHYYREWILPQLWIGINFDRLTLLALFDRNREILEMV 1007
 SPDLAAT-----YGPTEAAQKVIGHYYREWILPQLWIGINFDRLTLLALFDRNREILEMV 112
 SPDLQDAPLGQDNPSAASACKTROYVRYWILPFLWVGILFDRLTLLALFDRNREILEMV 416
 ----- 1

1030 1040 1050 1060 1070 1080
 NOV3 ref|XP_027243.1 172
 gi|15076843|gb| 1
 gi|6650377|gb|A 1067
 gi|13171105|gb| 172
 gi|7290294|gb|A 476
 ----- 1

LAVILATLVAFGLSILLIQCFFRDIIWVFQFCCLVIASCQYSLLKSVQPDSSSPRHGNRI 172
 LAVILATLVAFGLSILLIQCFFRDIIWVFQFCCLVIASCQYSLLKSVQPDSSSPRHGNRI 1067
 LAVVLAATLVAFGLSILLIQCFFRDIIWVFQFCCLVIASCQYSLLKSVQPDSSSPRHGNRI 172
 LAVVLAATLVAFGLSVLILLIQCFFRDIIWVFQFCCLVIASCQYSLLKSVQPDSSSPRHGNRI 476
 ----- 1

1090 1100 1110 1120 1130 1140
 NOV3 ref|XP_027243.1 232
 gi|15076843|gb| 1
 gi|6650377|gb|A 1127
 gi|13171105|gb| 232
 gi|7290294|gb|A 536
 ----- 1

AYSRPVYFCICCGLIWLLDYGSRNLTATKEKLYGITFTNLVFIASARDLIVVFTLCFPIV 232
 AYSRPVYFCICCGLIWLLDYGSRNLTATKEKLYGITFTNLVFIASARDLIVVFTLCFPIV 1127
 AYSRPVYFCICCGLIWLLDYGSRNLTISKEKLYCVTFNLVLIASARDLIVVFTLCFPIV 232
 AYSRPVYFCICCGLIWLLDYGSRNLTSSRFITLYCVALTSSLVIASARDLIVVFTLCFPIV 536
 ----- 1

1150 1160 1170 1180 1190 1200
 NOV3 ref|XP_027243.1 292
 gi|15076843|gb| 1
 gi|6650377|gb|A 1187
 gi|13171105|gb| 292
 gi|7290294|gb|A 596
 ----- 1

FFIGLLPVQNTFVMYLCEQLDIHIFGGNAATSLLAALYSEPCCSIVAVALLYGLCYGAED 292
 FFIGLLPVQNTFVMYLCEQLDIHIFGGNAATSLLAALYSEPCCSIVAVALLYGLCYGAED 1187
 FFIGLLPVQNTFVMYLCEQLDIHIFGGNAATSLLAALYSEPCCSIVAVALLYGLCYGAED 292
 FFVGLLPQVNTFVMYLFEQLDIHIFGGNAATSLLAALYSEPCCSIVAVALLYGLCYGAED 596
 ----- 1

1210 1220 1230 1240 1250 1260
 NOV3 ref|XP_027243.1 352
 gi|15076843|gb| 1
 gi|6650377|gb|A 1247
 gi|13171105|gb| 352
 gi|7290294|gb|A 656
 ----- 1

SWDGOHIPVLFSTFCGLLVAWSYHLSROSSDPSVLSSIVOSKIFPKTEPKNPEDPLSEVR 352
 SWDGOHIPVLFSTFCGLLVAWSYHLSRQSDPSVLFSIVOSKIFPKTEPKNPEDPLSEVR 1247
 SWDGOHIPVLFSTFCGLLVAWSYHLSRQSDPSVLFSIMOSKIFPKADEPKNPEDPLSEVR 352
 SWDGOHIPVLFSTFCGLLVAWSYHLSRQSDPSVLMMPLSKIFPKADEPKNPEDPLSEVR 656
 ----- 1

	1270	1280	1290	1300	1310	1320	
NOV3	DPLPEKLRNSVSERLQSDLIVVCIVIGVLYFAIHVSTVFTVLQPAKVKVLYALVCGFVGFM						412
ref XP_027243.1							1
gi 15076843 gb	DPLPEKLRNSVSERLQSDLIVVCIVIGVLYFAIHVSTVFTVLQPAKVKVLYALVCGFVGFM						1307
gi 6650377 gb A	DPLPEKLSNSVSERLQSDLIVVCIVIGVLYFAIHVSTVFTALQPAKVKVLYALVCGVVGAT						412
gi 13171105 gb	DPLPEKLRASVNERLQSDLIVVCIVIGVLYFAIHVSTVFTIALQPAKVKVLYALVCGVVGAT						716
gi 7290294 gb A							1
	1330	1340	1350	1360	1370	1380	
NOV3	HYVLPOVRKQLPWNCFSPHPLLKTLBYNQYEVRAAATMMWFEKDHWVLLFVEKNIIYPLIV						472
ref XP_027243.1							1
gi 15076843 gb	HYVLPOVRKQLPWNCFSPHPLLKTLBYNQYEVRAAATMMWFEKDHWVLLFVEKNIIYPLIV						1367
gi 6650377 gb A	HYVLPOVRKQLPWNCFSPRPLLRTABHSCQEVRRAAATMMWFEKDHWVLLFVEKNIIYPLIV						472
gi 13171105 gb	HYVLPOVRKQLPWNCFSPHPLLKTLBYNQYEVRAAATMMWFEKDHWVLLFVEKNIIYPLIV						776
gi 7290294 gb A							1
	1390	1400	1410	1420	1430	1440	
NOV3	LNELSSSAETIASPKRLNTELGALMITVAGLKLRLSSSSPTPYQYITVIFTVLFFKFDME						532
ref XP_027243.1							1
gi 15076843 gb	LNELSSSAETIASPKRLNTELGALMITVAGLKLRLSSSSPTPYQYITVIFTVLFFKFDME						1427
gi 6650377 gb A	LNELSSSAETIASPKRLNTELGALMITIAGLKLRLSSSSPTPYQYITVIFTVLFFKFDME						532
gi 13171105 gb	LNELSSCAREIASPKRLNTELGALMITVAGLKLRLSSSSPTPYQYITVIFTVLFFKFDME						836
gi 7290294 gb A							1
	1450	1460	1470	1480	1490	1500	
NOV3	AFSETMLLDLFFMSILPNKIKWELLYKLOFVYTYIAFWOITWGSAFHAFAOOPFAVPNSAML						592
ref XP_027243.1							1
gi 15076843 gb	AFSETMLLDLFFMSILPNKIKWELLYKLOFVYTYIAFWOITWGSAFHAFAOOPFAVPNSAML						1487
gi 6650377 gb A	AFSETMLLDLFFMSILFSKIKWELLYKLOFVYTYIAFWOITWGSAFHAFAOOPFAVPNSAML						592
gi 13171105 gb	HLSETMLLDLFFMSILFSKIKWELLYKLOFVYTYIAFWOITWGSAFHAFAOOPFAVPNSAML						896
gi 7290294 gb A							1
	1510	1520	1530	1540	1550	1560	
NOV3	FIQAVSIAFFSTPLNPLGLSAIFITSYVRPVKFWERDYI STKRVDHSNTRLASQDRNPGS						652
ref XP_027243.1							1
gi 15076843 gb	FIQAVSIAFFSTPLNPLGLSAIFITSYVRPVKFWERDYI STKRVDHSNTRLASQDRNPGS						1547
gi 6650377 gb A	FIQAVSIAFFSTPLNPLGLSAIFITSYVRPVKFWERDYI STKRVDHSNTRLASQDRNPGS						652
gi 13171105 gb	FIQAVSIAFFSTPLNPLGLSAIFITSYVRPVKFWERDYI STKRVDHSNTRLASQDRNPGS						956
gi 7290294 gb A	MSTPEESSSPDPSYT-SAVPVDCRVTDLK-----ENEMKOVEFDEDTRVLLIKON						47
	1570	1580	1590	1600	1610	1620	
NOV3	DDNNLNSISFYEHLTRSLQHSLCGDLLLLGRWGN I STGDCFI LASDYLNALVHLIEIGNGLV						712
ref XP_027243.1							1
gi 15076843 gb	DDNNLNSISFYEHLTRSLQHSLCGDLLLLGRWGN I STGDCFI LASDYLNALVHLIEIGNGLV						1607
gi 6650377 gb A	DDNNLNSISFYEHLTRSLQHSLCGDLLLLGRWGN I STGDCFI LASDYLNALVHLIEIGNGLV						712
gi 13171105 gb	DDNNLNSISFYEHLTRSLQHSLCGDLLLLGRWGN I STGDCFI LASDYLNALVHLIEIGNGLV						1016
gi 7290294 gb A	DRLLAVGAKCTHYAPQ T --CALGLGRVRCPWHGACFNL EYGDIEDFP -----GLD						97
	1630	1640	1650	1660	1670	1680	
NOV3	TFQLRGLEFRGTYCQQREVEAI TEGV EDEG FC CCCEPGHI PH ILSFNAAF FS QRWLAWEV V						772
ref XP_027243.1							1
gi 15076843 gb	TFQLRGLEFRGTYCQQREVEAI TEGV EDEG FC CCCEPGHI PH ILSFNAAF FS QRWLAWEV V						1667
gi 6650377 gb A	TFQLRGLEFRGTYCQQREVEAI TEGV EDEG FC CCCEPGHI PH ILSFNAAF FC QRWLAWEV V						772
gi 13171105 gb	TFQLRGLEFRGTYCQQREVEAI TEGV EDEG FC CCCEPGHI PH ILSFNAAF FC QRWLAWEV V						1076
gi 7290294 gb A	SLP-----CYRVE						105
	1690	1700	1710	1720	1730	1740	
NOV3	VTKYILEGYSITDNSAASMLQVF DLR IVLT TTYYVKGI YYV TISSKLEEWLAN TM QEGL						832
ref XP_027243.1							5
gi 15076843 gb	VTKYILEGYSITDNSAASMLQVF DLR IVLT TTYYVKGI YYV TISSKLEEWLAN TM QEGL						1727
gi 6650377 gb A	VTKYILEGYSITDNSAASMLQVF DLR IVLT TTYYVKGI YYV TISSKLEEWLAN TM QEGL						832
gi 13171105 gb	VTKYILEGYSITDNSAASMLQVF DLR IVLT TTYYVKGI YYV TISSKLEEWLAN TM QEGL						1136

gi|7290294|gb|A VG-----NEQQ-----VMLRAKRSDLVNNKRLKKNMV 131

		1750	1760	1770	1780	1790	1800		
5	NOV3	RLCADRNYVDVDPFTFNPN	-IDEYDHRLAGISRESFCVIYLWIEYCSSRRAKPVDVKD						
	ref XP_027243.1	RLCADRNYVDVDPFTFNPN	-IDEYDHRLAGISRESFCVIYLWIEYCSSRRAKPVDVKD					891	
	gi 15076843 gb	RLCADRNYVDVDPFTFNPN	-IDEYDHRLAGISRESFCVIYLWIEYCSSRRAKPVDVKD					64	
	gi 6650377 gb A	RLCADRNYVDVDPFTFNPN	-IDEYDHRLAGISRESFCVIYLWIEYCSSRRAKPVDVKD					1786	
10	gi 13171105 gb	RLCADRNYVDVDPFTFNPN	-IDEYDHRLAGISRESFCVIYLWIEYCSSRRAKPVDVKD					891	
	gi 7290294 gb A	RGCSEERNYVDVDPFTFNPN	-IDEYDHRLAGISRESFCVIYLWIEYCSSRRAKPVDVKD					1195	
		RKPKDDQRFVWVGGCGPSGAVAVETIRQEGFRGRLTIVCREDYLIPYDRVWISKAMNLIEP						191	
			1810	1820	1830	1840	1850	1860	
15	NOV3	SSLVTLCYGLCVLGRRALGTASHHMMSSNLESLFLYGLHALFKGDFRIS	S	RDEWI FADME					951
	ref XP_027243.1	SSLVTLCYGLCVLGRRALGTASHHMMSSNLESLFLYGLHALFKGDFRIS	S	RDEWI FADME					124
	gi 15076843 gb	SSLVTLCYGLCVLGRRALGTASHHMMSSNLESLFLYGLHALFKGDFRIS	S	RDEWI FADME					1846
	gi 6650377 gb A	SSLVTLCYGLCVLGRRALGTASHHMMSSNLESLFLYGLHALFKGDFRIS	S	RDEWI FADME					951
	gi 13171105 gb	SSLVTLCYGLCVLGRRALGTASHHMMSSNLESLFLYGLHALFKGDFRIS	S	RDEWI FADME					1255
20	gi 7290294 gb A	SSLVTLCYGLCVLGRRALGTASHHMMSSNLESLFLYGLHALFKGDFRIS	S	RDEWI FADME					237
		Q-----LRFR-----DEEFLKEYPLIPLQGVAAEKLDTAQXELHCNAGMIVVKYDKI							
			1870	1880	1890	1900	1910	1920	
25	NOV3	LRKVVVPGIRMSIK	LHQDHFTSPDEYDDPTVLYEAIVSHEKNLVIAHEGDPAWRSAVLA						1010
	ref XP_027243.1	LRKVVVPGIRMSIK	LHQDHFTSPDEYDDPTVLYEAIVSHEKNLVIAHEGDPAWRSAVLA						183
	gi 15076843 gb	LRKVVVPGIRMSIK	LHQDHFTSPDEYDDPTVLYEAIVSHEKNLVIAHEGDPAWRSAVLA						1905
	gi 6650377 gb A	LRKVVVPGIRMSIK	LHQDHFTSPDEYDDPTVLYEAIVSHEKNLVIAHEGDPAWRSAVLA						1010
	gi 13171105 gb	LRKVVVPGIRMSIK	LHQDHFTSPDEYDDPTVLYEAIVSHEKNLVIAHEGDPAWRSAVLA						1314
	gi 7290294 gb A	YLATGCSAFPPPIPVGVALENVRIVRELADUTKAMLASTTPES:							MVC 282
30			1930	1940	1950	1960	1970	1980	
	NOV3	NSPSSLALRHVMDDGTNEYKIIIMLNRRYLSFRVIKVNKECVRGLWACQQQELVFLRNRP							1070
	ref XP_027243.1	NSPSSLALRHVMDDGTNEYKIIIMLNRRYLSFRVIKVNKECVRGLWACQQQELVFLRNRP							243
35	gi 15076843 gb	NSPSSLALRHVMDDGTNEYKIIIMLNRRYLSFRVIKVNKECVRGLWACQQQELVFLRNRP							1965
	gi 6650377 gb A	NSPSSLALRHVMDDGTNEYKIIIMLNRRYLSFRVIKVNKECVRGLWACQQQELVFLRNRP							1070
	gi 13171105 gb	NSPSSLALRHVMDDGTNEYKIIIMLNRRYLSFRVIKVNKECVRGLWACQQQELVFLRNRP							1374
	gi 7290294 gb A	LGSSPVALEAAAGLVSKVQSYTWCRENPLVAFGAICORVFLQFEDNKVVMRMESG-							341
40	NOV3	ERGSIQNAKQALRNMINSSCDQPIGYPIFVSPLTTSYSDSHQQLKDILGGPISLGNIRNF							1130
	ref XP_027243.1	ERGSIQNAKQALRNMINSSCDQPIGYPIFVSPLTTSYSDSHQQLKDILGGPISLGNIRNF							303
	gi 15076843 gb	ERGSIQNAKQALRNMINSSCDQPIGYPIFVSPLTTSYSDSHQQLKDILGGPISLGNIRNF							2025
	gi 6650377 gb A	ERGSIQNAKQALRNMINSSCDQPIGYPIFVSPLTTSYSDSHQQLKDILGGPISLGNIRNF							1130
45	gi 13171105 gb	ERGSIQNAKQALRNMINSSCDQPIGYPIFVSPLTTSYSDSHQQLKDILGGPISLGNIRNF							1434
	gi 7290294 gb A	-IAEIVGNEDDGKVSEVLVDDTRUPCDILQGTCGSKLTQFLAKSGVKVNNGSVDVTPF							400
50	NOV3	IVSTWHLRLKGCGAGCNSSGGNIEDSDTGGTSCIGNNATTA	N	TANPHSNVIQGSIGNPGQCS					1190
	ref XP_027243.1	IVSTWHLRLKGCGAGCNSSGGNIEDSDTGGTSCIGNNATTA	N	TANPHSNVIQGSIGNPGQCS					363
	gi 15076843 gb	IVSTWHLRLKGCGAGCNSSGGNIEDSDTGGTSCIGNNATTA	N	TANPHSNVIQGSIGNPGQCS					2085
	gi 6650377 gb A	IVSTWHLRLKGCGAGCNSSGGNIEDSDTGGTSCIGNNATTA	N	TANPHSNVIQGSIGNPGQCS					1190
55	gi 13171105 gb	IVSTWHLRLKGCGAGCNSSGGNIEDSDTGGTSCIGNNATTA	N	TANPHSNVIQGSIGNPGQCS					1463
	gi 7290294 gb A	IVSTWHLRLKGCGAGCNSSGGNIEDSDTGGTSCIGNNATTA	N	TANPHSNVIQGSIGNPGQCS					421
			2110	2120	2130	2140	2150	2160	
60	NOV3	GIGLHPPVTSYPPTLGTSHSSHVSQSGLVRQSPARASVASOSS-	YCYSS-RHSSLRMTTT						1248
	ref XP_027243.1	GIGLHPPVTSYPPTLGTSHSSHVSQSGLVRQSPARASVASOSS-	YCYSS-RHSSLRMTTT						421
	gi 15076843 gb	GIGLHPPVTSYPPTLGTSHSSHVSQSGLVRQSPARASVASOSS-	YCYSS-RHSSLRMTTT						2143
	gi 6650377 gb A	GIGLHPPVTSYPPTLGTSHVSQSGLVRQSPARASVASOSS-	YCYSS-RHSSLRMTTT						1248
	gi 13171105 gb	-----LS-CGTSOSOSVQSGLVRQSPARASVASOSS-	YCYSS-RHSSLRMTTT						1511
65	gi 7290294 gb A	-----LAHDVRVIGHYQIAQYHGPVIAINMCG-----							448
			2170	2180	2190	2200	2210	2220	
70	NOV3	GFVPCCRSTSOSLRLPSSIQSRLSMVNQMEPSGCGSGACVQHGLPSSSSSSQSIPAC							1308
	ref XP_027243.1	GFVPCCRSTSOSLRLPSSIQSRLSMVNQMEPSGCGSGACVQHGLPSSSSSSQSIPAC							481
	gi 15076843 gb	GFVPCCRSTSOSLRLPSSIQSRLSMVNQMEPSGCGSGACVQHGLPSSSSSSQSIPAC							2203

	gi 6650377 gb A	GFVPCRRSSTSQISLRNLPPSIQSRLSMVNQOMEAASOCGJCCVOHGLPSSSSSQSIPAC	1308		
	gi 13171105 gb	GMEPCRRSSTSQISLRNLPPSIQSRLSMVNQOMEAASOCGJCCVOHGLPSSSSSQSIPAC	1558		
	gi 7290294 gb A	--G-----VKKLEAVPEFFTLIFGKG--WRYAG-----HG-----SYKDVIIDGEM	485		
5		2230 2240 2250 2260 2270 2280			
	NOV3	KHHTLVGFLATEGGQSSATDAC	PGNTLSPANNSHS	RKAEVIVYRVQIVDPSQIL	1361
	ref XP_027243.1	KHHTLVGFLATEGGQSSATDAC	PGNTLSPANNSHS	RKAEVIVYRVQIVDPSQIL	534
10	gi 15076843 gb	KHHTLVGFLATEGGQSSATDAC	PGNTLSPANNSHS	KKAEVIVYRVQIVDPSQIL	2256
	gi 6650377 gb A	KHHTLVFLGREGGCSEATAC	PGNTLSPANNSHS	RKAEVIVYRVQIVDPSQIL	1361
	gi 13171105 gb	KRHTLVGLGNDGCGTIVTEPLSQHHHHHHHHHQHNPATATVRRDDDISYRVQIVDVGQVL	G-----	1618	
	gi 7290294 gb A	BDFKFVAMFINEADTVAVASC	RDPIVAQFAELTSQGXCL	526	
15		2290 2300 2310 2320 2330 2340			
	NOV3	EGINLSKRKELOWPDEGIRLKAGRNSWKDWSPQEGLMEGHVIHRWVPCSRDPGTRSHIDKA	1421		
	ref XP_027243.1	EGINLSKRKELOWPDEGIRLKAGRNSWKDWSPQEGLMEGHVIHRWVPCSRDPGTRSHIDKA	594		
	gi 15076843 gb	EGINLSKRKELOWPDEGIRLKAGRNSWKDWSPQEGLMEGHVIHRWVPCSRDPGTRSHIDKA	2316		
20	gi 6650377 gb A	EGINLSKRKELHWPDGETRLKAGRNSWKDWSPQEGLMEGHVIHRWVPCSRDPGTRSHIDKA	1421		
	gi 13171105 gb	ENINLSKRKELOWPDDAYRKAGRTRQWWDSPPLEGLMEGHVIHRWVPCSRDPGSRSHIDKA	1678		
	gi 7290294 gb A	G-----RGQIEDP-----A-----REDWIKXLCQP-----LPQVR-----	552		
25		2350 2360			
	NOV3	VLLVQIDDKYVTVIETGVLELGAEV	1446		
	ref XP_027243.1	VLLVQIDDKYVTVIETGVLELGAEV	619		
	gi 15076843 gb	VLLVQIDDKYVTVIETGVLELGAEV	2341		
	gi 6650377 gb A	VLLVQIDDKYVTIETGVLELGAEV	1446		
	gi 13171105 gb	VLLVQIDDKYVTIETGVLELGAEV	1703		
30	gi 7290294 gb A	-----	552		

Pecanex gene was originally discovered in *Drosophila*, encoding a large, membrane-spanning protein. The mouse homolog was recently reported. In the absence of maternal expression of the pecanex gene, the embryo develops severe hyperneuralization similar to that characteristic of Notch mutant embryos. Early gastrula embryos, lacking both maternally and zygotically expressed activity of the neurogenic pecanex locus, are shown to contain a greater than wild-type number of stably determined neural precursor cells which can differentiate into neurons in culture. Therefore it is anticipated that this novel human pecanex will be involved in neuronal differentiation, maintenance of neuronal precursors and neurological diseases.

The disclosed NOV3 nucleic acid of the invention encoding a Human homolog of the *Drosophila* pecanex protein includes the nucleic acid whose sequence is provided in Table 3A or a fragment thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in Table 3A while still encoding a protein that maintains its Human homolog of the *Drosophila* pecanex activities and physiological functions, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are complementary to any of the nucleic acids just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way

gi 13653970 ref XP_009546.3 (XM_009546)	serine/threonine kinase 15 [Homo sapiens]	403	369/403 (91%)	381/403 (93%)	0.0
gi 4507275 ref NP_003591.1 (NM_003600)	serine/threonine kinase 15; Serine/threonine protein kinase 15 [Homo sapiens]	403	369/403 (91%)	380/403 (93%)	0.0
gi 7446411 pir JC5974	aurora-related kinase 1 (EC 2.7.---) - human	403	367/403 (91%)	379/403 (93%)	0.0
gi 4507279 ref NP_003149.1 (NM_003158)	serine/threonine kinase 6; Serine/threonine protein kinase-6; serine/threonine kinase 6 (aurora/IPL1-like) [Homo sapiens]	402	342/403 (84%)	360/403 (88%)	0.0

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 4D.

5

Table 4D. ClustalW Analysis of NOV4

- 1) NOV4 (SEQ ID NO:14)
 2) gi|12654873|gb|AAH01280.1|AAH01280 (BC001280) serine/threonine kinase 15 [Homo sapiens] (SEQ ID NO:47)
 10 3) gi|13653970|ref|XP_009546.3|(XM_009546) serine/threonine kinase 15 [Homo sapiens] (SEQ ID NO:48)
 4) gi|4507275|ref|NP_003591.1|(NM_003600) serine/threonine kinase 15; Serine/threonine protein kinase 15 [Homo sapiens] (SEQ ID NO:49)
 15 5) gi|7446411|pir||JC5974 aurora-related kinase 1 (EC 2.7.---) - human (SEQ ID NO:50)
 6) gi|4507279|ref|NP_003149.1|(NM_003158) serine/threonine kinase 6; Serine/threonine protein kinase-6; serine/threonine kinase 6 (aurora/IPL1-like) [Homo sapiens] (SEQ ID NO:51)

20

	10	20	30	40	50
NOV4
gi 12654873	MDSSENCISGPVAKNIPVGGPPVLTQQFPQCNPPLPANSGQAOQWVLCP				
gi 13653970	MDRSKENCISGPVKATAAPVGGPKRVLVTQQFPQCNPPLPVNSGQAOQWVLCP				
gi 4507275	MDRSKENCISGPVKATAAPVGGPKRVLVTQQFPQCNPPLPVNSGQAOQWVLCP				
gi 7446411	MDRSKENCISGPVKATAAPVGGPKRVLVTQQFPQCNPPLPVNSGQAOQWVLCP				
gi 4507279	MDRSKENCISGPVKATAAPVGGPKRVLVTQQFPQCNPPLPVNSGQAOQWVLCP				

30

	60	70	80	90	100
NOV4
gi 12654873	SNSSQRVPLOAQOKLVSSHKPVNQKQKQLQATSVPHPNSRPLNNNTQNSKQ				
gi 13653970	SNSSQRVPLOAQKLVSSHKPVNQKQKQLQATSVPHPNSRPLNNNTQNSKQ				
gi 4507275	SNSSQRVPLOAQKLVSSHKPVNQKQKQLQATSVPHPNSRPLNNNTQNSKQ				
gi 7446411	SNSSQRVPLOAQKLVSSHKPVNQKQKQLQATSVPHPNSRPLNNNTQNSKQ				

gi|4507279| SNSSQRVPLOAQKLVSSHCKPVQNQKQQLQATSVHPVSRPLNNTOKSKC

	110	120	130	140	150
5	NOV4 gi 12654873 gi 13653970 gi 4507275 gi 7446411 gi 4507279	SPISAPENNPEEEELASKQXNEESKKRQWALEDFEIGRPLGKGKFGNVYLA PLPSAPENNPEEEELASKQXNEESKKRQWALEDFEIGRPLGKGKFGNVYLA PLPSAPENNPEEEELASKQXNEESKKRQWALEDFEIGRPLGKGKFGNVYLA PLPSAPENNPEEEELASKQXNEESKKRQWALEDFEIGRPLGKGKFGNVYLA PLPSAPENNPEEEELASKQXNEESKKRQWALEDFEIGRPLGKGKFGNVYLA PLPSHILKIIILRRRNWHQNPK-MNQKEAVALEDFEIGRPLGKGKFGNVYLA			
10					
15	NOV4 gi 12654873 gi 13653970 gi 4507275 gi 7446411 gi 4507279	REKQSKFILALKVLFAQLEKAGVEHQLRREVEIQSHLRHPNIIRLYGYF REKQSKFILALKVLFAQLEKAGVEHQLRREVEIQSHLRHPNIIRLYGYF REKQSKFILALKVLFAQLEKAGVEHQLRREVEIQSHLRHPNIIRLYGYF REKQSKFILALKVLFAQLEKAGVEHQLRREVEIQSHLRHPNIIRLYGYF REKQSKFILALKVLFAQLEKAGVEHQLRREVEIQSHLRHPNIIRLYGYF REKQSKFILALKVLFAQLEKAGVEHQLRREVEIQSHLRHPNIIRLYGYF			
20					
25	NOV4 gi 12654873 gi 13653970 gi 4507275 gi 7446411 gi 4507279	HDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYTITELANALSYCHSK HDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYTITELANALSYCHSK HDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYTITELANALSYCHSK HDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYTITELANALSYCHSK HDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYTITELANALSYCHSK HDATRVYLILEYAPLGTVYRELQKLSKFDEORTANLYNRYANALSYCHSK			
30					
35	NOV4 gi 12654873 gi 13653970 gi 4507275 gi 7446411 gi 4507279	TVIHRDIKPENLLLGSAGELKIADFGWSVHAPSSRTTLCGTLDYLPPEM RVIHRDIKPENLLLGSAGELKIADFGWSVHAPSSRTTLCGTLDYLPPEM RVIHRDIKPENLLLGSAGELKIADFGWSVHAPSSRTTLCGTLDYLPPEM RVIHRDIKPENLLLGSAGELKIADFGWSVHAPSSRTTLCGTLDYLPPEM RVIHRDIKPENLLLGSAGELKIADFGWSVHAPSSRTTLCGTLDYLPPEM			
40					
45	NOV4 gi 12654873 gi 13653970 gi 4507275 gi 7446411 gi 4507279	IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPD IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPD IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPD IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPD IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPD			
50					
55	NOV4 gi 12654873 gi 13653970 gi 4507275 gi 7446411 gi 4507279	FVTEGARDLISRLLKHNPSQRPMMLREVLEHPWITANSSKPSNCQNKESAS FVTEGARDLISRLLKHNPSQRPMMLREVLEHPWITANSSKPSNCQNKESAS FVTEGARDLISRLLKHNPSQRPMMLREVLEHPWITANSSKPSNCQNKESAS FVTEGARDLISRLLKHNPSQRPMMLREVLEHPWITANSSKPSNCQNKESAS FVTEGARDLISRLLKHNPSQRPMMLREVLEHPWITANSSKPSNCQNKESAS			
60	NOV4 gi 12654873 gi 13653970 gi 4507275 gi 7446411 gi 4507279	KQS			
65					

Table 5B. NOV5 protein sequence (SEQ ID NO:16)

```

MGQSQGDGHGPRRGKIKDEKKKNKYEPLVPTRVAEKEEKTKGQDVASKLPLVTLHTQCRLKLLKLERIKDYLLM
VEEFIRNQEIQIKLLEEKQEEGRSKVDDLRGTPMSVGNLEEIIDDNHAIIVSTSVGSEHYDSIISFVEKDLEPGC
SILLRHVKHAVIGVLMDDTGPLVTMMKVEKAPQETYVNTGGLDNQIQEIKESMELPLPHPEYYEEMGTKPPKGV
ILCGPPGTGKTLAKAVANQTSATFLRVVGSeliQKYLGDGPKLVRQVFQVAEEHAPSIMFTDEIEAIGTKRYD
SNSGGEREIQQTMLELELLNQLGGFDSREDVKVIMATKVETLDPVLIRPGRIDKKIEFHLPDEKTKKHIFQIH
TSRMTLANDVTLDLIMAKDDFSGADIKAICTEAGLMLREHMRKATNEDFKKSIESVLYKKHEGIPEGLYL

```

The full amino acid sequence of the protein of the invention was found to have 383 of 442 amino acid residues (86%) identical to, and 405 of 442 amino acid residues (91%) similar to, the 440 amino acid residue ptnr:SWISSPROT-ACC:P49014 protein from *Mus musculus* (Mouse), and *Rattus norvegicus* (Rat) (26S Protease Regulatory Subunit 4 (P26S4) (E = 1.7e⁻²⁰⁰).

NOV5 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 5C.

Table 5C. BLAST results for NOV5

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 4506207 ref NP_02793.1 (NM_002802)	proteasome (prosome, macropain) 26S subunit, ATPase, 1; Proteasome 26S subunit, ATPase, 1 [Homo sapiens]	440	382/442 (86%)	405/442 (91%)	0.0
gi 6679501 ref NP_032973.1 (NM_008947)	protease (prosome, macropain) 26S subunit, ATPase 1 [Mus musculus]	440	383/442 (86%)	405/442 (90%)	0.0
gi 345717 pir A44468	26S proteasome regulatory chain 4 [validated] - human	440	381/442 (86%)	404/442 (91%)	0.0
gi 16741033 gb AAH16368.1 AAH16368 (BC016368)	protease (prosome, macropain) 26S subunit, ATPase 1 [Homo sapiens]	440	382/442 (86%)	404/442 (90%)	0.0
gi 2492516 sp Q90732 PRS4_CHICK	26S PROTEASE REGULATORY SUBUNIT 4 (P26S4)	440	378/442 (85%)	402/442 (90%)	0.0

10

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 5D.

Table 5D ClustalW Analysis of NOV5

- 1) NOV5 (SEQ ID NO:16)
 15 2) gi|4506207|ref|NP_002793.1| (NM_002802) proteasome (prosome, macropain) 26S
subunit, ATPase, 1; Proteasome 26S subunit, ATPase, 1 [Homo sapiens] (SEQ ID NO:52)
 3) gi|6679501|ref|NP_032973.1| (NM_008947) protease (prosome, macropain) 26S
subunit, ATPase 1 [Mus musculus] (SEQ ID NO:53)
 4) gi|345717|pir||A44468 26S proteasome regulatory chain 4 [validated] - human (SEQ
ID NO:54)

		5) gi 16741033 gb AAH16368.1 AAH16368 (BC016368) protease (prosome, macropain) 26S subunit, ATPase 1 (Homo sapiens) (SEQ ID NO:55)
5		
10		6) gi 2492516 sp Q90732 PRS4_CHICK 26S PROTEASE REGULATORY SUBUNIT 4 (P26S4) (SEQ ID NO:56)
15		
20		
25		
30		
35		
40		
45		
50		
55		
60		
65		
70		

Tables 5E-F list the domain description from DOMAIN analysis results against NOV5. This indicates that the NOV5 sequence has properties similar to those of other proteins known to contain this domain.

Table 5E. Domain Analysis of NOVs

gnl|Pfam|pfam00004, AAA, ATPase family associated with various cellular activities (AAA). AAA family proteins often perform chaperone-like functions that assist in the assembly, operation, or disassembly of protein complexes (SEQ ID NO:101)
CD-Length = 186 residues, 100.0% aligned
Score = 190 bits (483), Expect = 1e-49

Table 5F. Domain Analysis of NOVs

gnl|Smart|smart00382, AAA, ATPases associated with a variety of cellular activities; AAA. This profile/alignment only detects a fraction of this vast family. The poorly conserved N-terminal helix is missing from the alignment. (SEQ ID NO:102)
CD-Length = 151 residues, 100.0% aligned
Score = 61.6 bits (148), Expect = 9e-11

40 NOV 4: 218 PPKGVILCGPPGTGKTLAKAVANQTSATFLRVV-----GSELIQK 258
 | + | ++ || ||| + ||| || + || + | + |
 Sbjct: 1 PGEVVILVGPPGSGKTTLARALARELGPDGGVIYIDGEDLREEALLQLRLLVGEDK 60

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 6D.

Table 6D Clustal W Sequence Alignment

5	1) NOV6 (SEQ ID NO:18)
	2) gi 3077703 dbj BAA25784.1 (AB004816) mitsugumin29 [Oryctolagus cuniculus] (SEQ ID NO:57)
	3) gi 6678874 ref NP_032622.1 (NM_008596) mitsugumin 29 [Mus musculus] (SEQ ID NO:58)
10	4) gi 12836843 dbj BAB23831.1 (AK005132) putative [Mus musculus] (SEQ ID NO:59)
	5) gi 1351168 sp P20488 SYPH_BOVIN SYNAPTOPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) (SEQ ID NO:60)
	6) gi 2134413 pir I50720 synaptophysin IIa - chicken (SEQ ID NO:61)
15	10 20 30 40 50
	NOV6
	gi 3077703 MSSTESAGRTADKSPQQVDRLLIVGLRWRRLLEEPLGFIKVLOWLFAIFAF
	gi 6678874 MSSTESPSPRAADKSPQQVDRLLIVGLRWRRLLEEPLGFIKVLOWLFAIFAF
20	gi 12836843 MSSTESPGRTSDKSPQQVDRLLIVGLRWRRLLEEPLGFIKVLOWLFAIFAF
	gi 1351168 -----MDPVVSQASAGTFRALKPEPLAFLRALEELLFAMFAF
	gi 2134413 -----MDVVNCIVAGCQEPWVVKPEPLGFVKVLOWVFAIFAF
	-----MCMVIFAPLFAIFAF
25	60 70 80 90 100
	NOV6
	gi 3077703 GSCGSYSGETGAMVRQNNNEAKDVSSITIVLFGYPFRLHQVQYEMPLQDDEES
	gi 6678874 GSCGSYSGETGAMVRQNNNEAKDVSSITIVLFGYPFRLHQVQYEMPLQDODDS
30	gi 12836843 GSCGSYSGETGALVLVQNNNEAKDVSSITIVLFGYPFRLHQVQYEMPLQDODS
	gi 1351168 ATCCGGYSCLRLSVDCANKTISNSNLTIDIAFAYPFRLOCVTFEVPTGK-
	gi 2134413 ATCCGGYSCLRLSVDCANKTISNSDNLIDIAFAYPFRLHQVNTDAPTGK-
	ATCCGGYSCLRLSVDCANKTISNSDNLIDIAFAYPFRLHQVNTDAPTGK-
35	110 120 130 140 150
	NOV6
	gi 3077703 SSKTMILMGDFSAPAEFFVTLCIGIFSEFYTMAALVIVYDRFHNLTYENKRFP
	gi 6678874 SSKTMILMGDFSAPAEFFVTLCIGIFSEFYTMAALVIVYDRFHKLTYENKRFP
40	gi 12836843 TSKTMILMGDFSAPAEFFVTLCIGIFSEFYTMAALVIVYDRFHKLTYENKRFP
	gi 1351168 EQQKILALVGDSSSSAEFFFVTVAVFAFLYSLAAITVIVYIFFONKYRENNRGP
	gi 2134413 DPKKDFLVGNYSSSAEFFFVTVAVFAFLYSMGALATYIFLONKYRENNYGP
	RRRFSLSLIGDFSSSAEFFFVTVAVFAFLYSLAAITVIVYIFFONKYRENNFGP
45	160 170 180 190 200
	NOV6
	gi 3077703 LVDFCVTVSFIFEWLVAAAAWGKGLTDVKCATRESSITAAMSVCHEAV
	gi 6678874 LVDFCVTVSFIFEWLVAAAAWGKGLTDVKCATRESSITAAMSVCHEAV
50	gi 12836843 LVDFCVTVSFIFEWLVAAAAWGKGLTDVKCATRESSITAAMSVCHEAV
	gi 1351168 LIIDFIVTVVFSPFLWLGSSAWAKGLSDVKVATDFKEVLLIMSPCKQPSNK
	gi 2134413 MLDFLATAVFAFMWLVSAAWAKGLSDVKMADPENIIKGHIVCHOPGNT
	LIIDFIVTVVFSPFLWLGSSAWAKGLSDVKIATDPDEVLLIMSAACKQPSNK
55	210 220 230 240 250
	NOV6
	gi 3077703 CSAGAATPSMGLANLISVLFGFPINFLWAGNCWFVFKETIPWHCGCGQDQDQ
	gi 6678874 CSAGAATPSMGLANLISVLFGFPINFLWAGNCWFVFKETIPWHCGCGQ-
60	gi 12836843 CSAGAATPSMGLANLISVLFGFPINFLWAGNCWFVFKETIPWHCGCGQ-
	gi 1351168 CWAVHSPPMSSLNTSVVFGRDNFILWAGNWFVFKETGWSSGORYLSDP
	gi 2134413 CKELRDPVTGLNTSVVFGRDNFILWAGNWFVFKETGWAAFLRAPPGA
	CLPPVRSPPMSSLNTSVVFGRDNFILWAGNWFVFKETGWSSGORYHAADT
65	260 270 280 290 300
	NOV6
	gi 3077703 DDO-----GQGP-----SQESAAEQG-----
	gi 6678874 --DO-----GQGP-----SQESAAEQG-----
70	gi 12836843 --DO-----GQGP-----SQESAAEQG-----
	gi 1351168 MEKH-----SSSYNCG-----RYN-----QESYGSGGYS-----QQAN-----
	PFKCPAPGDAYGQAGYGGCGGGYGPQPSYGPQGGYQPDYGQPASSGGGY

	gi 2134413	M EK C-----SSGYNOC-GYN-ODSYGPAGGYN---QPGS----Y
		310 320
5	NOV6
	gi 3077703	----- ----- ----- -----
	gi 6678874	----- ----- ----- -----
	gi 12836843	GPTSDEFQQQP---SGPTSFNNCI
10	gi 1351168	GPQQ-DYGQQQGYGPQQGAPTSFSNOM
	gi 2134413	GQVG-DYGQPQSYYGQSGPTSFANCI

Table 6E lists the domain description from DOMAIN analysis results against NOV6. This indicates that the NOV6 sequence has properties similar to those of other proteins known to contain this domain.

Table 6E. Domain Analysis of NOV6

gnl|Pfam|pfam01284, Synaptophysin, Synaptophysin / synaptoporin. (SEQ ID NO:103)
CD-Length = 298 residues, 70.8% aligned
Score = 244 bits (622), Expect = 6e-66

In skeletal muscle, excitation-contraction (E-C) coupling requires the conversion of the depolarization signal of the invaginated surface membrane, namely the transverse (T-) tubule, to Ca²⁺ release from the sarcoplasmic reticulum (SR) (Takeshima H et al., Biochem J 1998 Apr 1;331 (Pt 1):317-22 / PMID: 9512495, UI: 98180964). Signal transduction occurs at the junctional complex between the T-tubule and SR, designated as the triad junction, which contains two components essential for E-C coupling, namely the dihydropyridine receptor as the T-tubular voltage sensor and the ryanodine receptor as the SR Ca²⁺-release channel. However, functional expression of the two receptors seemed to constitute neither the signal-transduction system nor the junction between the surface and intracellular membranes in cultured cells, suggesting that some as-yet-unidentified molecules participate in both the machinery. In addition, the molecular basis of the formation of the triad junction is totally

Table 7B. Encoded NOV7 protein sequence (SEQ ID NO:20).

```
LTGREVLTTPFPGLGTAAPAQGGAAHKQCDLLKLSRRQKQLCRRPGLAETLRDAAHLGLECFQFRHERWNCS
LEGRMGLLKRGFKETAFLYAVSSAALTHTLARACSGRMERCTCDDSPGLESRQAWQWGVCGDNLKYSTKFLSNF
LGSKRGNKDLRARAHDHNTVGIKAKVKSGLRTCKCHGVSGSCAVRTCWKQLSPFRETGQVLKLRYDSAVKVSSA
TNEALGRLELWAPARQGSLTKGLAPRSGLVYMEDSPSFCRPSKYSPTAGRVCSEACSSLCCGRGYDTQSR
VAFSCHCQVQWCCYECQQCVQEELVYTCKH
```

The disclosed NOV7 amino acid sequence has 205 of 330 amino acid residues (62%) identical to, and 252 of 330 amino acid residues (76%) similar to, the 354 amino acid residue ptnr:SWISSPROT-ACC:O42280 protein from *Gallus gallus* (Chicken) (WNT-14 Protein Precursor) ($E = 1.3e^{-114}$).

The tissue expression of NOV7 is predicted to be expressed in brain because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:AF031168|acc:AF031168.1) a closely related *Gallus gallus* Wnt-14 protein (Wnt-14) mRNA, complete cds homolog.

NOV7 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 7C.

Table 7C. BLAST results for NOV7

Gene Index/Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 16303264 dbj BAB70499.1 (AB063483)	WNT14B [Homo sapiens]	357	330/331 (99%)	330/331 (99%)	e-175
gi 3915306 sp O42280 WN14_CHICK	WNT-14 PROTEIN PRECURSOR	354	204/332 (61%)	253/332 (75%)	e-109
gi 15082261 ref NP_003386.1 (NM_003395)	wingless-type MMTV integration site family, member 14 [Homo sapiens]	365	209/335 (62%)	255/335 (75%)	e-108
gi 139748 sp P10108 WNT1_XENLA	WNT-1 PROTEIN PRECURSOR (XWNT-1) (XINT-1)	371	120/313 (38%)	175/313 (55%)	5e-58
gi 3024851 sp O14905 WN15_HUMAN	WNT-15 PROTEIN	120	120/120 (100%)	120/120 (100%)	2e-56

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 7D.

Table 7D Information for the ClustalW proteins

- 1) NOV7 (SEQ ID NO:20)
- 2) gi|16303264|dbj|BAB70499.1| (AB063483) WNT14B [Homo sapiens] (SEQ ID NO:62)
- 3) gi|3915306|sp|O42280|WN14_CHICK WNT-14 PROTEIN PRECURSOR (SEQ ID NO:63)
- 4) gi|15082261|ref|NP_003386.1| (NM_003395) wingless-type MMTV integration site family, member 14 [Homo sapiens] (SEQ ID NO:64)
- 5) gi|139748|sp|P10108|WNT1_XENLA WNT-1 PROTEIN PRECURSOR (XWNT-1) (XINT-1) (SEQ ID NO:65)
- 6) gi|3024851|sp|O14905|WN15_HUMAN WNT-15 PROTEIN (SEQ ID NO:66)



5 gi|16303264| -----MRPPP ALA GLC LAL PAA RAS YFGLTGRE -----VLTPFPEL
 gi|3915306| -----M ALL RALL LG --I IACTPRPSA RYFGLTCNE -----ALTILP-L
 gi|15082261| MLDGSPLARWL AAA FGL TLL LAALRPSA RYFGLTCSE -----PLTILP-L
 gi|139748| -----M RILTFLLGKTEWVLAFS ELS NTIAVNNSGKWWGIVAVVASAG
 gi|3024851| -----
 NOV7
 10 gi|16303264| GTAAA PAQGAHLKOC DILKLISRROKOLCRREPGLAETLFDNAHIGLLEC
 gi|3915306| GTAAA PAQGAHLKOC DILKLISRROKOLCRREPGLAETLFDNAHIGLLEC
 gi|15082261| TSEMEAAVKAHYKVCDRLKLEKKORRMCRD P GCAETLMDAISMSALEC
 gi|139748| TLEP-EAAQAHYKACDRKLKEKRRMCRD P GVAETLVEAVMSALEC
 gi|3024851| NVLPGSDARPVPLVLDPSIQLLSROKRITRNPCTILOSITRGLHSIREC
 NOV7
 15 gi|16303264| QEQFRH ERWNCSLEG -R MG -LLKRGFKETAFLYAVSSAALTHM ARAC
 gi|3915306| QEQFRH ERWNCSLEG -RTG -LLKRGFKETAFLYAVSSAALTHM ARAC
 gi|15082261| QYQFRFERWNCTLEG RYRAS -LLKRGFKETAFLYATSSAGLTHAMAKAC
 gi|139748| QEQFRFERWNCTLEG RYRAS -LLKRGFKETAFLYATSSAGLTHALAKAC
 gi|3024851| KWHFRNRWNQPTGTGNQVFGKLTNGC RETA FVFAITSSAGVTHSVARSC
 NOV7
 25 gi|16303264| SAGR MER CT CDDSPGLESRCQAWQWGVC GDNLKYSKTFI S N F L G S K R G N K D
 gi|3915306| SAGR MER CT CDDSPGLESRCQAWQWGVC GDNLKYSKTFI S N F L G S K R G N K D
 gi|15082261| SAGR MER CT CDEAPDLBAPRPAWQWGCGDNLKYSNKFVKEFLC-RKP KND
 gi|139748| SAGR MER CT CDEAPDLBAPRPAWQWGCGDNLKYS SKFVKEFLC-RKP KND
 gi|3024851| SEGSIESCSDYRRRGPGGPDWHWGCCSDNIEFGRFIGRBPVDSSERCRD
 NOV7
 35 gi|16303264| LRARADAHNT HVG IKA VSKGURTTCKCHGVSGSCAVRTC W K Q L S P F R E I C
 gi|3915306| LRARADAHNT HVG IKA VSKGURTTCKCHGVSGSCAVRTC W K Q L S P F R E I C
 gi|15082261| LRARVDDEHNNLVGMVKVIAKG VETTCKCHGVSGSCAVRTC W R Q L A P F H E V C
 gi|139748| LRARVDDEHNNLVGMVKVIAKG VETTCKCHGVSGSCAVRTC W R Q L A P F H E V C
 gi|3024851| LKYLVLPHNNQACR LTM TEM RQE CKCHGMSGSCSLRTCWMLRPPFRSVC
 SGSCAVRTC W K Q L S P F R E I C
 NOV7
 45 gi|16303264| OVLKL RYDS AVKVSSA TNEALC RLE LWA PAR --- QGS LTKGLA PRSC D LV
 gi|3915306| OVLKL RYDS AVKVSSA TNEALC RLE LWA PAR --- QGS LTKGLA PRSC D LV
 gi|15082261| KOLKOKVETSLKVGS TNEA TGE -GDI SPKK--KSI PGHSDQIPRIT IDLV
 gi|139748| KHLKHKVETALKVG S TNEA AGE AGAI S P P R GRAS CAGG SDPL P R I P L V
 gi|3024851| DALKDREDCASKV T Y S N N E S N R W G S R S D P H --L E P E N P T H A L P S S O D L V
 OVLKL RYDS AVKVSSA TNEALC RLE LWA PAR --- QGS LTKGLA PRSC D LV
 NOV7
 55 gi|16303264| YMEDSPSPFCRPSKYS -PGTAGRVCSRE --- ASC S LCC G R G Y D T Q S R I
 gi|3915306| YMEDSPSPFCRPSKYS -PGTAGRVCSRE --- ASC S LCC G R G Y D T Q S R I
 gi|15082261| YIDDSPSPFCI M S R Y S -PGT SGR K CY M --- KNC S I C C G R G H N T O S R V
 gi|139748| YFEKSPNPFCS P S E K N G T P G T I G R I C H S T S L G L D G C E L L C C G R G Y R S I A E K
 gi|3024851| YMEDSPSPFCRPSKYS -PGTAGRVCSRE --- ASC S LCC G R G Y D T Q S R I
 NOV7
 60 gi|16303264| VAFSCHCQV WCCY VEC Q C V O D E L V Y T C K H
 gi|3915306| VAFSCHCQV WCCY VEC Q C V O D E L V Y T C K H
 gi|15082261| VTRPCQCOV RWC CY VEC Q C T Q R E E V Y T C K D
 gi|139748| VTERCHC T F N W C C V T Q N C T S S O I V E C L -
 gi|3024851| VAFSCHCQV ---

VEAWSMSALECQFQFRFERWNCTLEGRYRASLLKRGFKETAFLYAISSAGLTHALAKACSAGRMRERCTCDE
 APDLENREGWKWGGCSIEDIEFGGMVSREFADARENRPDARSAMNRHNNEAGRQVIKAGVETTCKCHGVSGS
 CTVRTCWRQLAPFHEVGKHLKHKEYSALKVGSTTNEAGEAGAISPPRGRASGAGSDPLPRTPELVHLD
 SPSFCLAGRFSPTAGRRCHREKNCEISCCGRGHNTQSRRVTRPCQCQVRWCYVECRQCTQREEVYTCKG

The disclosed NOV8 amino acid sequence has 270 of 354 amino acid residues (76%) identical to, and 310 of 354 amino acid residues (87%) similar to, the 354 amino acid residue ptnr:SWISSPROT-ACC:O42280 protein from *Gallus gallus* (Chicken) (WNT-14 Protein Precursor ($1.2e^{-151}$)).

NOV8 is expressed in at least brain. This information was derived by determining the tissue sources of the sequences that were included in the invention including but not limited to SeqCalling sources, Public EST sources, Literature sources, and/or RACE sources.

In addition, the sequence is predicted to be expressed in brain because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:AF031168|acc:AF031168.1) a closely related [*Gallus gallus* Wnt-14 protein (Wnt-14) mRNA, complete cds].

NOV8 also has homology to the amino acid sequence shown in the BLASTP data listed in Table 8C.

Table 8C. BLAST results for NOV8

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 15082261 ref NP_003386.1 (NM_003395)	wingless-type MMTV integration site family, member 14 [Homo sapiens]	365	306/340 (90%)	321/340 (94%)	e-167
gi 3915306 sp O42280 WN14_CHICK	WNT-14 PROTEIN PRECURSOR	354	270/357 (75%)	310/357 (86%)	e-142
gi 16303264 dbj BAB70499.1 (AB063483)	WNT14B [Homo sapiens]	357	193/339 (56%)	244/339 (71%)	e-100
gi 7106447 ref NP_033548.1 (NM_009522)	wingless-related MMTV integration site 3A [Mus musculus]	352	141/311 (45%)	179/311 (57%)	2e-62
gi 5821261 dbj BAA83743.1 (AB024080)	Wnt-3a [Gallus gallus]	376	139/311 (44%)	179/311 (56%)	3e-62

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The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 8D.

Table 8D. Information for the ClustalW proteins

- 1) NOV8 (SEQ ID NO:22)
- 2) gi|15082261|ref|NP_003386.1| (NM_003395) wingless-type MMTV integration site family, member 14 [Homo sapiens] (SEQ ID NO:64)
- 3) gi|3915306|sp|O42280|WN14_CHICK WNT-14 PROTEIN PRECURSOR (SEQ ID NO:63)
- 4) gi|16303264|dbj|BAB70499.1| (AB063483) WNT14B [Homo sapiens] (SEQ ID NO:62)
- 5) gi|7106447|ref|NP_033548.1| (NM_009522) wingless-related MMTV integration site 3A [Mus musculus] (SEQ ID NO:67)
- 6) gi|5821261|dbj|BAA83743.1| (AB024080) Wnt-3a [Gallus gallus] (SEQ ID NO:68)

		10	20	30	40	50
		-M-A-L-Y-S-T-I-G-V-V-C-T-	-C-D-P-S-Y-F-G-L-T-G-S-E-P-L-T-I-L-P-		
5	NOV8		M-L-D-G-S-P-L-A-R-W-L-A-R-A-F-G-L-T-I-L-L-A-A-L-R-	-P-E-B-A-Y-F-G-L-T-G-S-E-P-L-T-I-L-P-		
	g1 15082261	M-L-D-G-S-P-L-A-R-W-L-A-R-A-F-G-L-T-I-L-L-A-A-L-R-	-P-E-B-A-Y-F-G-L-T-G-S-E-P-L-T-I-L-P-			
	g1 3915306		-M-U-L-R-R-U-L-L-C-L-L-A-C-T-P-	-R-P-E-B-A-Y-F-G-L-T-G-N-E-A-L-T-I-L-P-		
	g1 16303264	-M-R-P-P-M-A-L-A-G-C-L-L-A-L-P-	-A-A-B-E-Y-F-G-L-T-G-E-R-E-V-L-T-P-F-E-G-			
	g1 7106447	-M-A-P-L-G-Y-L-L-X-L-C-E-	-L-K-Q-A-	-L-C-S-M-P-W-W-S-		
	g1 5821261	-M-K-S-P-C-E-V-W-A-K-E-R-I-G-L-K-Q-W-G-C-G-W-T-P-M-C-S-A-N-K-K-W-I-S-E-Q-R-E-S-L-E-L-W				
10		60	70	80	90	100
	NOV8
	g1 15082261	-L-T-G-S-P-B-A-N-A-C-A-H-Y-N-A-C-D-R-U-K-	-L-E-R-K-O-R-R-M-C-R-R-D-P-G-V-A-E-T-I-V-E-A-V-S			
	g1 3915306	-L-T-G-S-P-B-A-N-A-C-A-H-Y-N-A-C-D-R-U-K-	-L-E-R-K-O-R-R-M-C-R-R-D-P-G-V-A-E-T-I-V-E-A-V-S			
15	g1 16303264	-L-T-S-E-M-E-B-E-Y-K-A-H-Y-V-C-D-R-U-K-	-L-E-K-O-R-R-M-C-R-R-D-P-G-A-E-T-I-M-E-A-I-S			
	g1 7106447	-L-G-T-A-A-P-A-O-O-G-A-H-I-K-O-C-P-L-U-X-T-S-K-R-O-K-O-L-C-R-R-E-P-G-I-A-E-T-I-R-D-O-A-H				
	g1 5821261	-L-A-V-G-P-O-Y-S-S-L-S-T-Q-P-L-I-C-A-S-T-P-G-I-V-F-K-C-O-U-F-C-R-N-Y-V-E-I-M-P-S-V-A-E-C-V-K	D-V-G-S-I-A-L-G-H-O-Y-S-S-L-G-T-Q-P-I-L-C-S-W-P-G-I-V-F-K-C-O-U-F-C-R-N-Y-V-E-I-M-P-S-V-A-E-C-V-K			
20		110	120	130	140	150
	NOV8
	g1 15082261	-M-S-A-L-E-C-O-Q-F-R-F-E-R-W-N-C-T-L-E-G-R--Y-P-A-S-L-L-K-R-C-F-K-E-T-A-F-L-Y-A-I-S-S-A-G-L-T	-M-S-A-L-E-C-O-Q-F-R-F-E-R-W-N-C-T-L-E-G-R--Y-P-A-S-L-L-K-R-C-F-K-E-T-A-F-L-Y-A-I-S-S-A-G-L-T			
	g1 3915306	-M-S-A-L-E-C-O-Q-F-R-F-E-R-W-N-C-T-L-E-G-R--Y-P-A-S-L-L-K-R-C-F-K-E-T-A-F-L-Y-A-I-S-S-A-G-L-T	-M-S-A-L-E-C-O-Q-F-R-F-E-R-W-N-C-T-L-E-G-R--Y-P-A-S-L-L-K-R-C-F-K-E-T-A-F-L-Y-A-I-S-S-A-G-L-T			
25	g1 16303264	-G-L-L-E-C-C-O-Q-F-R-H-E-R-W-N-C-T-L-E-G-R--R-I-G-L-L-K-R-C-F-K-E-T-A-F-L-Y-A-U-S-S-A-A-L-T	-G-L-L-E-C-C-O-Q-F-R-H-E-R-W-N-C-T-L-E-G-R--R-I-G-L-L-K-R-C-F-K-E-T-A-F-L-Y-A-U-S-S-A-A-L-T			
	g1 7106447	-A-G-I-C-E-C-C-O-H-F-F-R-G-R-W-N-C-T-F-V-S-N-S-L-A-I-F-G-P-V-I-D-K-A-T-R-E-S-A-F-V-H-A-I-S-A-G-V-A	-A-G-I-C-E-C-C-O-H-F-F-R-G-R-W-N-C-T-F-V-S-N-S-L-A-I-F-G-P-V-I-D-K-A-T-R-E-S-A-F-V-H-A-I-S-A-G-V-A			
	g1 5821261	-E-G-I-C-E-C-C-O-H-F-F-R-G-R-W-N-C-T-F-V-N-D-S-L-A-I-F-G-P-V-I-D-K-A-T-R-E-S-A-F-V-H-A-I-S-A-G-V-A	-E-G-I-C-E-C-C-O-H-F-F-R-G-R-W-N-C-T-F-V-N-D-S-L-A-I-F-G-P-V-I-D-K-A-T-R-E-S-A-F-V-H-A-I-S-A-G-V-A			
30		160	170	180	190	200
	NOV8
	g1 15082261	H-A-L-U-K-A-C-S-A-G-R-M-E-R-C-T-C-D-E-A-P-D-L-E-N-R-E-A-W-W-G-C-C-S-E-D-Y-E-P-G-G-M-V-S-R-E-F-A-D	H-A-L-U-K-A-C-S-A-G-R-M-E-R-C-T-C-D-E-A-P-D-L-E-N-R-E-A-W-W-G-C-C-S-E-D-Y-E-P-G-G-M-V-S-R-E-F-A-D			
	g1 3915306	H-A-L-U-K-A-C-S-A-G-R-M-E-R-C-T-C-D-E-A-P-D-L-E-N-R-E-A-W-W-G-C-C-S-E-D-Y-E-P-G-G-M-V-S-R-E-F-A-D	H-A-L-U-K-A-C-S-A-G-R-M-E-R-C-T-C-D-E-A-P-D-L-E-N-R-E-A-W-W-G-C-C-S-E-D-Y-E-P-G-G-M-V-S-R-E-F-A-D			
	g1 16303264	H-T-L-A-R-A-C-S-A-G-R-M-E-R-C-T-C-D-E-A-S-F-G-E-L-E-S-R-O-W-W-G-V-C-G-D-N-L-K-Y-S-N-K-F-V-K-E-E-L-G	H-T-L-A-R-A-C-S-A-G-R-M-E-R-C-T-C-D-E-A-S-F-G-E-L-E-S-R-O-W-W-G-V-C-G-D-N-L-K-Y-S-N-K-F-V-K-E-E-L-G			
	g1 7106447	F-A-M-T-R-S-C-A-B-G-S-A-A-I-C-G-C-S-S-R-L-Q-G-S-P-G-E-C-H-W-G-C-C-S-E-D-Y-E-P-G-G-M-V-S-R-E-F-A-D	F-A-M-T-R-S-C-A-B-G-S-A-T-I-C-G-C-E-T-R-H-K-G-S-P-G-E-C-H-W-G-C-C-S-E-D-Y-E-P-G-G-M-V-S-R-E-F-A-D			
	g1 5821261	F-A-M-T-R-S-C-A-B-G-S-A-T-I-C-G-C-E-T-R-H-K-G-S-P-G-E-C-H-W-G-C-C-S-E-D-Y-E-P-G-G-M-V-S-R-E-F-A-D	F-A-M-T-R-S-C-A-B-G-S-A-T-I-C-G-C-E-T-R-H-K-G-S-P-G-E-C-H-W-G-C-C-S-E-D-Y-E-P-G-G-M-V-S-R-E-F-A-D			
40		210	220	230	240	250
	NOV8
	g1 15082261	A-R-D-N-T-P-D-A-R-S-A-M-T-R-H-N-N-E-A-G-R-O-V-I-L-K-A-C-V-E-T-T-C-K-C-H-G-V-S-G-S-C-I-V-R-T-C-H-I-Q-L	A-R-D-N-T-P-D-A-R-S-A-M-T-R-H-N-N-E-A-G-R-O-V-I-L-K-A-C-V-E-T-T-C-K-C-H-G-V-S-G-S-C-I-V-R-T-C-H-I-Q-L			
	g1 3915306	R-P-S-S-K-C-U-R-A-R-V-D-P-H-N-N-L-V-G-V-V-N-I-L-K-A-C-V-E-T-T-C-K-C-H-G-V-S-G-S-C-I-V-R-T-C-H-I-Q-L	R-P-S-S-K-C-U-R-A-R-V-D-P-H-N-N-L-V-G-V-V-N-I-L-K-A-C-V-E-T-T-C-K-C-H-G-V-S-G-S-C-I-V-R-T-C-H-I-Q-L			
	g1 16303264	R-K-P-N-H-C-U-R-A-R-V-D-P-H-N-N-L-V-G-V-V-N-I-L-K-A-C-V-E-T-T-C-K-C-H-G-V-S-G-S-C-I-V-R-T-C-H-I-Q-L	R-K-P-N-H-C-U-R-A-R-V-D-P-H-N-N-L-V-G-V-V-N-I-L-K-A-C-V-E-T-T-C-K-C-H-G-V-S-G-S-C-I-V-R-T-C-H-I-Q-L			
	g1 7106447	S-K-R-G-N-K-C-U-R-A-R-V-D-H-N-T-H-V-G-I-K-A-V-K-S-C-U-R-T-T-C-K-C-H-G-V-S-G-S-C-A-V-R-T-C-H-I-Q-L	S-K-R-G-N-K-C-U-R-A-R-V-D-H-N-T-H-V-G-I-K-A-V-K-S-C-U-R-T-T-C-K-C-H-G-V-S-G-S-C-A-V-R-T-C-H-I-Q-L			
	g1 5821261	A-R-G-N-F-P-C-A-R-S-A-M-T-R-H-N-N-E-A-G-R-O-A-T-A-S-H-H-L-K-C-K-C-H-G-U-S-G-S-C-P-U-K-T-C-H-I-Q-S-Q	A-R-G-N-F-P-C-A-R-S-A-M-T-R-H-N-N-E-A-G-R-O-A-T-A-S-H-H-L-K-C-K-C-H-G-U-S-G-S-C-P-U-K-T-C-H-I-Q-S-Q			
45		260	270	280	290	300
	NOV8
	g1 15082261	A-P-P-E-B-V-C-H-L-L-N-K-Y-E-S-A-U-K-V-G-S-T-T-N-E-A-C-E-A-G-A-I-S-P-P-R-G-A-S-G-A-G-G-S-D-P-	A-P-P-E-B-V-C-H-L-L-N-K-Y-E-S-A-U-K-V-G-S-T-T-N-E-A-C-E-A-G-A-I-S-P-P-R-G-A-S-G-A-G-G-S-D-P-			
	g1 3915306	A-P-P-E-B-V-C-H-L-L-N-K-Y-E-S-A-U-K-V-G-S-T-T-N-E-A-C-E-A-G-A-I-S-P-P-R-G-A-S-G-A-G-G-S-D-P-	A-P-P-E-B-V-C-H-L-L-N-K-Y-E-S-A-U-K-V-G-S-T-T-N-E-A-C-E-A-G-A-I-S-P-P-R-G-A-S-G-A-G-G-S-D-P-			
	g1 16303264	S-P-R-H-P-I-C-K-L-O-K-Y-E-T-S-U-K-V-G-S-T-T-N-E-A-T-E-E-G-D-I-S-P-P-K--K-S-I-P-G-H-S-D-O-I	S-P-R-H-P-I-C-K-L-O-K-Y-E-T-S-U-K-V-G-S-T-T-N-E-A-T-E-E-G-D-I-S-P-P-K--K-S-I-P-G-H-S-D-O-I			
	g1 7106447	S-P-P-R-E-T-G-O-V-L-K-D-K-Y-D-S-A-S-E-M-V-V-E-K-H-R-E-S-R-G-W-V-E-T-L-R-P-R--Y---T-Y-F-K-A	S-P-P-R-E-T-G-O-V-L-K-D-K-Y-D-S-A-S-E-M-V-V-E-K-H-R-E-S-R-G-W-V-E-T-L-R-P-R--Y---T-Y-F-K-A			
	g1 5821261	P-D-E-R-T-G-O-V-L-K-D-K-Y-D-S-A-S-E-M-V-V-E-K-H-R-E-S-R-G-W-V-E-T-L-R-P-R--Y---N-F-F-K-A	P-D-E-R-T-G-O-V-L-K-D-K-Y-D-S-A-S-E-M-V-V-E-K-H-R-E-S-R-G-W-V-E-T-L-R-P-R--Y---N-F-F-K-A			
55		310	320	330	340	350
	NOV8
	g1 15082261	P-R-O-P-E-L-V-I-H-D-D-S-P-S-F-C-L-A-G--R-E-S-P-G-T-A-G-R-C-R-H-E-K-N--G-E-S-I-C-C-G-R-G	P-R-O-P-E-L-V-I-H-D-D-S-P-S-F-C-L-A-G--R-E-S-P-G-T-A-G-R-C-R-H-E-K-N--G-E-S-I-C-C-G-R-G			
	g1 3915306	P-R-O-P-E-L-V-I-H-D-D-S-P-S-F-C-L-A-G--R-E-S-P-G-T-A-G-R-C-R-H-E-K-N--G-E-S-I-C-C-G-R-G	P-R-O-P-E-L-V-I-H-D-D-S-P-S-F-C-L-A-G--R-E-S-P-G-T-A-G-R-C-R-H-E-K-N--G-E-S-I-C-C-G-R-G			
60	g1 16303264	P-R-S-G-D-L-V-Y-I-H-D-D-S-P-S-F-C-R-P--R-E-S-P-G-T-S-G-R-K-C-Y-D-K-N--G-E-S-I-C-C-G-R-G	P-R-S-G-D-L-V-Y-I-H-D-D-S-P-S-F-C-R-P--R-E-S-P-G-T-S-G-R-K-C-Y-D-K-N--G-E-S-I-C-C-G-R-G			
	g1 7106447	F-T-E-R-D-L-V-Y-Y-E-A-S-P-N-F-C-E-P-N-P-E-T-C-S-F-G-T-D-R-N-T-O-V-S-S-G-I-D-G-G-D-L-L-C-C-G-R-G	F-T-E-R-D-L-V-Y-Y-E-A-S-P-N-F-C-E-P-N-P-E-T-C-S-F-G-T-D-R-N-T-O-V-S-S-G-I-D-G-G-D-L-L-C-C-G-R-G			
	g1 5821261	S-T-E-K-D-L-V-Y-Y-E-A-S-P-N-F-C-E-P-N-P-E-T-C-S-F-G-T-I-R-D-F-I-C-A-V-T-S-G-I-D-G-G-D-L-L-C-C-G-R-G	S-T-E-K-D-L-V-Y-Y-E-A-S-P-N-F-C-E-P-N-P-E-T-C-S-F-G-T-I-R-D-F-I-C-A-V-T-S-G-I-D-G-G-D-L-L-C-C-G-R-G			
65		360	370	380		
	NOV8		
	g1 15082261	H-N-T-O-S-R-V-W-T-R-P-C-O-C-O-V-R-N-C-C-Y-V-E-C-O-R-C-O-T-R-E-E-V-Y-T-C-H-G	H-N-T-O-S-R-V-W-T-R-P-C-O-C-O-V-R-N-C-C-Y-V-E-C-O-R-C-O-T-R-E-E-V-Y-T-C-H-G			
	g1 3915306	H-N-T-O-S-R-V-W-T-R-P-C-O-C-O-V-R-N-C-C-Y-V-E-C-O-R-C-O-T-R-E-E-V-Y-T-C-H-G	H-N-T-O-S-R-V-W-T-R-P-C-O-C-O-V-R-N-C-C-Y-V-E-C-O-R-C-O-T-R-E-E-V-Y-T-C-H-G			
70	g1 16303264	V-D-T-O-S-R-L-V-A-F-S-O-L-C-O-V-W-N-C-C-Y-V-E-C-O-C-O-T-R-E-E-V-Y-T-C-H-G	H-N-A-V-U-B-E-R-R-E-K-O-H-C-O-V-H-N-C-C-Y-V-S-C-O-E-C-I-D-V-Y-D-W-H-T-C-H-			
	g1 7106447	H-N-A-V-U-B-E-R-R-E-K-O-H-C-O-V-H-N-C-C-Y-V-S-C-O-E-C-I-D-V-Y-D-W-H-T-C-H-	H-N-T-K-V-B-K-R-K-E-K-O-H-C-I-F-H-N-C-C-Y-V-R-C-O-E-C-I-D-V-Y-D-W-H-T-C-H-			
	g1 5821261	H-N-T-K-V-B-K-R-K-E-K-O-H-C-I-F-H-N-C-C-Y-V-R-C-O-E-C-I-D-V-Y-D-W-H-T-C-H-	H-N-T-K-V-B-K-R-K-E-K-O-H-C-I-F-H-N-C-C-Y-V-R-C-O-E-C-I-D-V-Y-D-W-H-T-C-H-			

The disclosed NOV9 polypeptide has homology to the amino acid sequences shown in the BLASTP data listed in Table 9C.

Table 9C. BLAST results for NOV9					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
.ptnr:pir-id:A53791	beta-adrenergic-receptor kinase (EC 2.7.1.126) 1 - human	689	495/497 (99%)	495/497 (99%)	0.0
ptnr:SWISSPROT-ACC:P25098	Beta-adrenergic receptor kinase 1 (EC 2.7.1.126)	689	494/497 (99%)	495/497 (99%)	0.0
ptnr:SPTREMBL-ACC:Q99LL8	SIMILAR TO ADRENERGIC, BETA, RECEPTOR KINASE 1 - Mus musculus	687	490/495 (98%)	493/495 (99%)	0.0
ptnr:SWISSPROT-ACC:P26817	Beta-adrenergic receptor kinase 1	689	489/497 (98%)	493/497 (99%)	0.0
ptnr:SPTREMBL-ACC:Q99MK8	G PROTEIN RECEPTOR KINASE 2	689	490/497 (98%)	494/497 (99%)	0.0

5 The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 9D. In the ClustalW alignment of the NOV9 proteins, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and
10 can potentially be altered to a much broader extent without altering protein structure or function.

Table 9D. ClustalW Analysis of NOV9

15	1) NOV9 (SEQ ID NO:24) 2) ptnr:pir-id:A53791 beta-adrenergic-receptor kinase (EC 2.7.1.126) 1 (SEQ ID NO:69) 3) ptnr:SWISSPROT-ACC:P25098 Beta-adrenergic receptor kinase 1 (EC 2.7.1.126) (SEQ ID NO:70) 4) ptnr:SPTREMBL-ACC:Q99LL8 SIMILAR TO ADRENERGIC, BETA, RECEPTOR KINASE 1 - Mus musculus (Mouse) (SEQ ID NO:71) 5) 6) ptnr:SWISSPROT-ACC:P26817 Beta-adrenergic receptor kinase 1 (EC 2.7.1.126) (Beta-ARK-1) (SEQ ID NO:72)
25	NOV9 MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIERSVMOKYLEDRGEVTFEKIFS 60 A53791 MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIERSVMOKYLEDRGEVTFEKIFS 60 P25098 MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIERSVMOKYLEDRGEVTFEKIFS 60 Q99LL8 --DLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIERSVMOKYLEDRGEVTFEKIFS 58 P26817 MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIERSVMOKYLEDRGEVTFEKIFS 60
30	NOV9 QKLGYLLFRDFCLNHLLEARPLVVFYEEIKKYEKLETEEERVARSREIFDSYINKELLAC 120 A53791 OKLGYLLFRDFCLNHLLEARPLVVFYEEIKKYEKLETEEERVARSREIFDSYINKELLAC 120

	P25098	QKLGYLLFRDFCLNHLEEARPLVEFYEEIKYEKLETEEERVARSREIFDSYIMKELLAC	120
	Q99LL8	QKLGYLLFRDFCLNHLEEA K PLVEFYEEIKYEKLETEEERVARSREIFDSYIMKELLAC	118
	P26817	QKLGYLLFRDFYI N HLEEA K PLVEFYEEIKYEKLETEEERVARSREIFDSYIMKELLAC	120
5	NOV9	SHPFSSKATEHVQGHLGKKQVPPDLFQPYIEEICONLRGDVFKQFIESDKFTRFQCQWKNV	180
	A53791	SHPFSSKATEHVQGHLGKKQVPPDLFQPYIEEICONLRGDVFKQFIESDKFTRFQCQWKNV	180
	P25098	SHPFSSKATEHVQGHLGKKQVPPDLFQPYIEEICONLRGDVFKQFIESDKFTRFQCQWKNV	180
	Q99LL8	SHPFSSKATEHVQGHLVKKQVPPDLFQPYIEEICONLRGDVFKQFIESDKFTRFQCQWKNV	178
	P26817	SHPFSSKATEHVQGHLVKKQVPPDLFQPYIEEICONLRGDVFKFIESDKFTRFQCQWKNV	180
10	NOV9	ELNIHLMNDFSVHRIIGRGGFGEVYGCRKADTGKMYAMKCLDKRKIKMKQGETLALNER	240
	A53791	ELNIHLMNDFSVHRIIGRGGFGEVYGCRKRDGTGKMYAMKCLDKRKIKMKQGETLALNER	240
	P25098	ELNIHLMNDFSVHRIIGRGGFGEVYGCRKRDGTGKMYAMKCLDKRKIKMKQGETLALNER	240
	Q99LL8	ELNIHLMNDFSVHRIIGRGGFGEVYGCRKADTGKMYAMKCLDKRKIKMKQGETLALNER	238
	P26817	ELNIHLMNDFSVHRIIGRGGFGEVYGCRKADTGKMYAMKCLDKRKIKMKQGETLALNER	240
15	NOV9	IMLSLVSTGDCPFIVCMSSYAFHTPDKLSFILDLMNGGLDHYSQHGVFSEADMRFYAAE	300
	A53791	IMLSLVSTGDCPFIVCMSSYAFHTPDKLSFILDLMNGGLDHYSQHGVFSEADMRFYAAE	300
	P25098	IMLSLVSTGDCPFIVCMSSYAFHTPDKLSFILDLMNGGLDHYSQHGVFSEADMRFYAAE	300
20	Q99LL8	IMLSLVSTGDCPFIVCMSSYAFHTPDKLSFILDLMNGGLDHYSQHGVFSEADMRFYAAE	298
	P26817	IMLSLVSTGDCPFIVCMSSYAFHTPDKLSFILDLMNGGLDHYSQHGVFSEADMRFYAAE	300
25	NOV9	IILGLEHMHNRFVVYRDLKPANILDEHGHRVISDLGLACDFSKKKPHASVGTHGYMAPE	360
	A53791	IILGLEHMHNRFVVYRDLKPANILDEHGHRVISDLGLACDFSKKKPHASVGTHGYMAPE	360
	P25098	IILGLEHMHNRFVVYRDLKPANILDEHGHRVISDLGLACDFSKKKPHASVGTHGYMAPE	360
	Q99LL8	IILGLEHMHNRFVVYRDLKPANILDEHGHRVISDLGLACDFSKKKPHASVGTHGYMAPE	358
	P26817	IILGLEHMHNRFVVYRDLKPANILDEHGHRVISDLGLACDFSKKKPHASVGTHGYMAPE	360
30	NOV9	VLQKGVAYDSSADWFSLGCMFLKLLRGHSPFRQHKTDKHEIDRMTLTMAVELPDSFSPE	420
	A53791	VLQKGVAYDSSADWFSLGCMFLKLLRGHSPFRQHKTDKHEIDRMTLTMAVELPDSFSPE	420
	P25098	VLQKGVAYDSSADWFSLGCMFLKLLRGHSPFRQHKTDKHEIDRMTLTMAVELPDSFSPE	420
	Q99LL8	VLQKGVAYDSSADWFSLGCMFLKLLRGHSPFRQHKTDKHEIDRMTLTMAVELPDSFSPE	418
	P26817	VLQKGVAYDSSADWFSLGCMFLKLLRGHSPFRQHKTDKHEIDRMTLTMAVELPDSFSPE	420
35	NOV9	LRSLLEGLLQRDVNRLGCLGRGAQEVKESPFFRSLDWOMVFQKYPPLIPPRGEVNAA	480
	A53791	LRSLLEGLLQRDVNRLGCLGRGAQEVKESPFFRSLDWQMVFQKYPPLIPPRGEVNAA	480
	P25098	LRSLLEGLLQRDVNRLGCLGRGAQEVKESPFFRSLDWQMVFQKYPPLIPPRGEVNAA	480
	Q99LL8	LRSLLEGLLQRDVNRLGCLGRGAQEVKESPFFRSLDWQMVFQKYPPLIPPRGEVNAA	478
	P26817	LRSLLEGLLQRDVNRLGCLGRGAQEVKESPFFRSLDWQMVFQKYPPLIPPRGEVNAA	480
40	NOV9	DAFDIGSFDEEDTKGIK-----QEVAVTFDTINAETDRLEAR	519
	A53791	DAFDIGSFDEEDTKGIKLLDSDQELYRNFPPLTISERWQQEVAVTFDTINAETDRLEAR	540
	P25098	DAFDIGSFDEEDTKGIKLLDSDQELYRNFPPLTISERWQQEVAVTFDTINAETDRLEAR	540
	Q99LL8	DAFDIGSFDEEDTKGIKLLDSDQELYRNFPPLTISERWQQEVAVTFDTINAETDRLEAR	538
	P26817	DAFDIGSFDEEDTKGIKLLDSDQELYRNFPPLTISERWOOEVAVTFDTINAETDRLEAR	540
45	NOV9	KAKNKQLGHEEDYALGKDCIMHGYMSKMNPFLTQWQRYYFYLFPNRLEWRGEAPEQSL	579
	A53791	KAKNKQLGHEEDYALGKDCIMHGYMSKMNPFLTQWQRYYFYLFPNRLEWRGEAPEQSL	600
	P25098	KAKNKQLGHEEDYALGKDCIMHGYMSKMNPFLTQWQRYYFYLFPNRLEWRGEAPEQSL	600
50	Q99LL8	KAKNKQLGHEEDYALGKDCIVHGYMSKMNPFLTQWQRYYFYLFPNRLEWRGEAPEQSL	598
	P26817	KAKNKQLGHEEDYALGKDCIMHGYMSKMNPFLTQWQRYYFYLFPNRLEWRGEAPEQSL	600
55	NOV9	LTMEEIQSVEETQIKERKCLLLKIRGGKOFILQCDSDPELVQWKELRDAYREAQQLVQR	639
	A53791	LTMEEIQSVEETQIKERKCLLLKIRGGKOFILQCDSDPELVQWKELRDAYREAQQLVQR	660
	P25098	LTMEEIQSVEETQIKERKCLLLKIRGGKOFILQCDSDPELVQWKELRDAYREAQQLVQR	660
	Q99LL8	LTMEEIQSVEETQIKERKCLLLKIRGGKOFVLQCDSDPELVQWKELRDAYREAQQLVQR	658
	P26817	LTMEEIQSVEETQIKERKCLLLKIRGGKOFVLQCDSDPELVQWKELRDAYREAQQLVQR	660
60	NOV9	VPKMKNPKRSPVVELSKVPLVQRGSANGL	668
	A53791	VPKMKNPKRSPVVELSKVPLVQRGSANGL	689
	P25098	VPKMKNPKRSPVVELSKVPLVQRGSANGL	689
	Q99LL8	VPKMKNPKRSPVVELSKVPLVQRGSANGL	687
	P26817	VPKMKNPKRSPVVELSKVPLVQRGSANGL	689

65 Tables 9E-9L list the domain descriptions from DOMAIN analysis results against NOV9. This indicates that the NOV9 sequence has properties similar to those of other proteins known to contain this domain.

Table 10C. BLAST results for NOV10

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
ptnr:SPTREMBL- ACC:Q9UL64	ALPHA MANNOSIDASE 6A8B - Homo sapiens	1062	763/771 (99%)	767/771 (99%)	0.0
ptnr:SPTREMBL- ACC:Q9NTJ4	HYPOTHETICAL 115.8 KDA PROTEIN - Homo sapiens	1040	715/722 (99%)	718/722 (99%)	0.0
ptnr:TREMBLNEW- ACC:AAH16253	SIMILAR TO MANNOSIDASE, ALPHA, CLASS 2C, MEMBER 1	1039	635/730 (89%)	692/730 (94%)	0.0
ptnr:SWISSPROT- ACC:P21139	Alpha-mannosidase (EC 3.2.1.24)	1040	625/731 (85%)	661/731 (90%)	0.0
ptnr:SPTREMBL- ACC:Q13358	ALPHA-MANNOSIDASE - Homo sapiens	425	425/425 (100%)	425/425 (100%)	0.0

The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 10D. In the ClustalW alignment of the NOV10 protein, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.

Table 10D. ClustalW Analysis of NOV10

10	1) NOV10 (SEQ ID NO:26)				
15	2) ptnr: ALPHA MANNOSIDASE 6A8B - Homo sapiens (SEQ ID NO:73)				
20	3) ptnr: HYPOTHETICAL 115.8 KDA PROTEIN - Homo sapiens (SEQ ID NO:74)				
25	4) ptnr: SIMILAR TO MANNOSIDASE, ALPHA, CLASS 2C, MEMBER 1 (SEQ ID NO:75)				
30	5) ptnr: Alpha-mannosidase (EC 3.2.1.24) (SEQ ID NO:76)				
35	NOV10 Q9UL64 Q9NTJ4 AAH16253 P21139	M-A-A-A-P-F-L-K-H-Y- R-T-T-F-E-R-V-E-K-F-P-V-S-P-I-Y-F-T-D-Q-N-L-R-G-R-L-F-C-A-S-C-P-V-A-V-L-S-S-F-L-T-P-E-R-L-P-Y-Q-E-A-V-Q-R-T-P-F-R-P-A-Q-V-G M-A-A-A-P-F-L-K-H-Y- R-T-T-F-E-R-V-E-K-F-P-V-S-P-I-Y-F-T-D-Q-N-L-R-G-R-L-F-C-A-S-C-P-V-A-V-L-S-S-F-L-T-P-E-R-L-P-Y-Q-E-A-V-Q-R-T-P-F-R-P-A-Q-V-G M-A-A-A-P-F-L-K-H-Y- R-T-T-F-E-R-V-E-K-F-P-V-S-P-I-Y-F-T-D-Q-N-L-R-G-R-L-F-C-A-S-C-P-V-A-V-L-S-S-F-L-T-P-E-R-L-P-Y-Q-E-A-V-Q-R-T-P-F-R-P-A-Q-V-G M-A-A-A-P-F-L-K-H-Y- R-T-T-F-E-R-V-E-K-F-P-V-S-P-I-Y-F-T-D-Q-N-L-R-G-R-L-F-C-A-S-C-P-V-A-V-L-S-S-F-L-T-P-E-R-L-P-Y-Q-E-A-V-Q-R-T-P-F-R-P-A-Q-V-G M-A-A-A-P-F-L-K-H-Y- R-T-T-F-E-R-V-E-K-F-P-V-S-P-I-Y-F-T-D-Q-N-L-R-G-R-L-F-C-A-S-C-P-V-A-V-L-S-S-F-L-T-P-E-R-L-P-Y-Q-E-A-V-Q-R-T-P-F-R-P-A-Q-V-G		FRPAQVG 70 FRPAQVG 70 FRPAQVG 70 FRPAQVG 69 FRPAQVG 79	
40	NOV10 Q9UL64 Q9NTJ4 AAH16253 P21139	D-S-F-G-P-T-W-W-T-C-W- F-R-V-E-L-T-I-P-E-A-W-V-Q-E-V-H-L-C-W-E- S-D-G-E-C-L-V-W-R-D- S-E-P-V-Q-G-L-T-P- E-G-E-K-T-S-V-L-I- T-D-R-L-G-E-R-D-P-P D-S-F-G-P-T-W-W-T-C-W- F-R-V-E-L-T-I-P-E-A-W-V-Q-E-V-H-L-C-W-E- S-D-G-E-C-L-V-W-R-D- S-E-P-V-Q-G-L-T-P- E-G-E-K-T-S-V-L-I- T-D-R-L-G-E-R-D-P-P D-S-F-G-P-T-W-W-T-C-W- F-R-V-E-L-T-I-P-E-A-W-V-Q-E-V-H-L-C-W-E- S-D-G-E-C-L-V-W-R-D- S-E-P-V-Q-G-L-T-P- E-G-E-K-T-S-V-L-I- T-D-R-L-G-E-R-D-P-P D-S-F-G-P-T-W-W-T-C-W- F-R-V-E-L-T-I-P-E-A-W-V-Q-E-V-H-L-C-W-E- S-D-G-E-C-L-V-W-R-D- S-E-P-V-Q-G-L-T-P- E-G-E-K-T-S-V-L-I- S-E-R-L-P-A-S-D-P-P D-S-F-G-P-T-W-W-T-C-W- F-R-V-E-L-T-I-P-E-A-W-V-Q-E-V-H-L-C-W-E- S-D-G-E-C-L-V-W-R-D- S-E-P-V-Q-G-L-T-P- E-G-E-K-T-S-V-L-I- T-T-R-N-Q-F-S-P-A-Q-V-G 140 140 140 139 159		140 140 140 139 159	
NOV10 Q9UL64 Q9NTJ4 AAH16253 P21139	S-L-T-L-Y-V-E-V-A-N-G-L-L-G-A-G-K-G-S-W- I-A-A-P-D-P-E-K-M-F- Q-L-S-R-A-F-L-A-V-F- H-R-D-V-H-M-L-L-V-E- L-E-I-L-L-G-I-A-K-G-L-G-D-V-R-S-F-C S-L-T-L-Y-V-E-V-A-N-G-L-L-G-A-G-K-G-S-W- I-A-A-P-D-P-E-K-M-F- Q-L-S-R-A-F-L-A-V-F- H-R-D-V-H-M-L-L-V-E- L-E-I-L-L-G-I-A-K-G-L-G-D-V-R-S-F-C S-L-T-L-Y-V-E-V-A-N-G-L-L-G-A-G-K-G-S-W- I-A-A-P-D-P-E-K-M-F- Q-L-S-R-A-F-L-A-V-F- H-R-D-V-H-M-L-L-V-E- L-E-I-L-L-G-I-A-K-G-L-G-D-V-R-S-F-C S-L-T-L-Y-V-E-V-A-N-G-L-L-G-A-G-K-G-S-W- I-A-A-P-D-P-E-K-M-F- Q-L-S-R-A-F-L-A-V-F- H-R-D-V-H-M-L-L-V-E- L-E-I-L-L-G-I-A-K-G-L-G-D-V-R-S-F-C S-L-T-L-Y-V-E-V-A-N-G-L-L-G-A-G-K-G-S-W- I-A-A-P-D-P-E-K-M-F- Q-L-S-R-A-F-L-A-V-F- H-R-D-V-H-M-L-L-V-E- L-E-I-L-L-G-I-A-K-G-L-G-D-V-R-S-F-C		200 211 211 210 229		
NOV10 Q9UL64 Q9NTJ4 AAH16253 P21139	A-L-Y-T-A-N-O-M-V-W- C-D-P-A-Q-P-E-T-D-P-V-A-C-A-L-A-S-R-F-F-G-Q-H-G-G-E-S-Q-I-T-H-A-G-C-H-I-D-T-A-W-L-N-P-K-E-T-V-R-K-C-A-R-S-W-T-A-D-O-L-M-E-R-N-P A-L-Y-T-A-N-O-M-V-W- C-D-P-A-Q-P-E-T-D-P-V-A-C-A-L-A-S-R-F-F-G-Q-H-G-G-E-S-Q-I-T-H-A-G-C-H-I-D-T-A-W-L-N-P-K-E-T-V-R-K-C-A-R-S-W-T-A-D-O-L-M-E-R-N-P A-L-Y-T-A-N-O-M-V-W- C-D-P-A-Q-P-E-T-D-P-V-A-C-A-L-A-S-R-F-F-G-Q-H-G-G-E-S-Q-I-T-H-A-G-C-H-I-D-T-A-W-L-N-P-K-E-T-V-R-K-C-A-R-S-W-T-A-D-O-L-M-E-R-N-P A-L-Y-T-A-N-O-M-V-W- C-D-P-A-Q-P-E-T-D-P-V-A-C-A-L-A-S-R-F-F-G-Q-H-G-G-E-S-Q-I-T-H-A-G-C-H-I-D-T-A-W-L-N-P-K-E-T-V-R-K-C-A-R-S-W-T-A-D-O-L-M-E-R-N-P		291 291 290 229		
NOV10 Q9UL64	----- A-Q-O-L-E-W-V/K-S-R-Y-P-G-L-Y-S-R-I-Q-E-F-A-C-R-G-O-F-V/P-V-G-G-T-W-V-E-M-O-G/L-P-S-G-E-A-M-V-R-O-F-L-O-G-O/F-F-L-O-E-F-G-H-N-C-S-E-F-W-L-P		272		
NOV10 Q9UL64	E-F-I-F-A-C-S-O-N-C-O-L-E-W-V/K-S-R-Y/I-C-L-Y-S-R-I-Q-E-F-A-C-R-G-O-F-V/P-V-G-G-T-W-V-E-M-O-G/L-P-S-G-E-A-M-V-R-O-F-L-O-G-O/F-F-L-O-E-F-G-H-N-C-S-E-F-W-L-P		371		

		Q9NTJ4	[REDACTED]	371
		AAH16253	[REDACTED]	370
		P21139	[REDACTED]	281
5		NOV10	[REDACTED]	352
		Q9UL64	[REDACTED]	451
		Q9NTJ4	[REDACTED]	450
		AAH16253	[REDACTED]	314
		P21139	[REDACTED]	
10		NOV10	[REDACTED]	432
		Q9UL64	[REDACTED]	531
		Q9NTJ4	[REDACTED]	531
		AAH16253	[REDACTED]	530
		P21139	[REDACTED]	325
15		NOV10	[REDACTED]	512
		Q9UL64	[REDACTED]	611
		Q9NTJ4	[REDACTED]	611
		AAH16253	[REDACTED]	610
		P21139	[REDACTED]	365
20		NOV10	[REDACTED]	592
		Q9UL64	[REDACTED]	691
		Q9NTJ4	[REDACTED]	691
		AAH16253	[REDACTED]	690
		P21139	[REDACTED]	374
25		NOV10	[REDACTED]	672
		Q9UL64	[REDACTED]	771
		Q9NTJ4	[REDACTED]	771
		AAH16253	[REDACTED]	770
		P21139	[REDACTED]	402
30		NOV10	[REDACTED]	752
		Q9UL64	[REDACTED]	851
		Q9NTJ4	[REDACTED]	851
		AAH16253	[REDACTED]	850
		P21139	[REDACTED]	408
35		NOV10	[REDACTED]	912
		Q9UL64	[REDACTED]	1011
		Q9NTJ4	[REDACTED]	1011
		AAH16253	[REDACTED]	1010
		P21139	[REDACTED]	408
40		NOV10	[REDACTED]	833
		Q9UL64	[REDACTED]	931
		Q9NTJ4	[REDACTED]	931
		AAH16253	[REDACTED]	930
		P21139	[REDACTED]	
45		NOV10	[REDACTED]	833
		Q9UL64	[REDACTED]	931
		Q9NTJ4	[REDACTED]	931
		AAH16253	[REDACTED]	930
		P21139	[REDACTED]	
50		NOV10	[REDACTED]	963
		Q9UL64	[REDACTED]	1062
		Q9NTJ4	[REDACTED]	1040
		AAH16253	[REDACTED]	1039
		P21139	[REDACTED]	408
55		NOV10	[REDACTED]	
		Q9UL64	[REDACTED]	
		Q9NTJ4	[REDACTED]	
		AAH16253	[REDACTED]	
		P21139	[REDACTED]	
60		NOV10	[REDACTED]	
		Q9UL64	[REDACTED]	
		Q9NTJ4	[REDACTED]	
		AAH16253	[REDACTED]	
		P21139	[REDACTED]	

Table 10E lists the domain description from DOMAIN analysis results against NOV10. This indicates that the NOV10 sequence has properties similar to those of other proteins known to contain this domain.

Table 10E. Domain Analysis of NOV10			
Model	Description	Score	E-value
Glyco_hydro_38 (InterPro)	Glycosyl hydrolases family 38 (SEQ ID NO:111)	140.5	1e-39
Glyco_hydro_38: domain 1 of 2, from 230 to 332: score 89.2, E = 5.4e-25			
AC058790_d	230 VGGTWWVEMDGNLPSGEAMVRQFLQGQNFFLQEFG--KMCSEFWLPDT 274		
AC058790_d	275 FGYSAQLPQIM-HCGIRRFLTKLSWNLVNSFPHHT--PFWE---GLD 317		

functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.

Table 11F. ClustalW Analysis of NOV11

תְּמִימָנָה וְמִתְּמִימָנָה. כַּאֲשֶׁר בְּמִזְבֵּחַ

Q9ESN4	AIAQDADONYDYASNSVILHLGDEVFIKLDGGKHGGNSNKYSTFSGFIIVSD---	258
P02746	TFCDYAYNTEQVTIIGGMVVLKLECCENVFLQATDKNSLLCMEGANSIFSGFLLFPDMEA	251
AAH08983	TFCDYAYNTEQVTIIGGMVVLKLECCENVFLQATDKNSLLCMEGANSIFSGFLLFPDMEA	253

5

Tables 11E-11F list the domain descriptions from DOMAIN analysis results against NOV11. This indicates that the NOV11 sequence has properties similar to those of other proteins known to contain this domain.

Table 11E. Domain Analysis of NOV11

gn1|Smart|smart00110, C1Q, Complement component C1q domain.; Globular domain found in many collagens and eponymously in complement C1q. When part of full length proteins these domains form a 'bouquet' due to the multimerization of heterotrimers. The C1q fold is similar to that of tumour necrosis factor. (SEQ ID NO:104)
CD-Length = 132 residues, 99.2% aligned
Score = 113 bits (283), Expect = 1e-26

	Query:	108	PRIAFYAGL--RRPHEGYEVLRPDDVVNVGNAYEAASGKFTCPMPGVYFFAVHVLMRGG	165
	Sbjct:	2	+ + + + ++ + + + + +	
15	Query:	166	PRSAFSVIRSTNRPPPGQPVRFDKVLYNQQGHYPSTGKFTCPVPGVYYFSYHIESK--	59
	Sbjct:	60	++ + + + + + +	
	Query:	225	DGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDDGGKVHG-GNT	224
20	Sbjct:	119	-GRNVKVSLMKNGIQVMRECDEYQKGLYQVASGGALLQLRQGDQVLELDDKKNGLYAGE	118
	Query:	238	NKYSTFSGPIIYPD	
	Sbjct:	132	+ + +	

25

Table 11F. Domain Analysis of NOV11

gnl|Pfam|pfam00386, C1q, C1q domain. C1q is a subunit of the C1 enzyme complex that activates the serum complement system. (SEQ ID NO:112)
CD-Length = 125 residues, 100.0% aligned
Score = 102 bits (253), Expect = 3e-23

	Query:	111	AFYAGLRL-RPHEGYEVLRFDDVVNTNVGNAYEAAASGKFTCPMPGVYFFPAYHVLMRGGDGTS	169
	Sbjct:	1	AFTAIRSTRPPAPGQPVIFDEVLYNQQGHYDPATGKFTCPVPGLYYFNFHVSSK--GTN	57
30	Query:	170	MWADLMKNGQVRASAAIAQDADQNYYDASYNSVILHLDVGDEVFIKLDGKGKVG--GNTNKY	227
	Sbjct:	58	VCVSLMRNGVPVMSFCDEYAKGTYQVASGGAVLQLRQGDRVWLELDDKQTNGLLGGEGVH	117
35	Query:	228	STFSGFII 235	
	Sbjct:	118	SVFSGFL 125	

The first component of complement system is a calcium-dependent complex of the 3 subcomponents C1q, C1r, and C1s. Subcomponent C1q binds to immunoglobulin complexes

ptnr:SPTREMBL- ACC:P70208	PLEXIN 3 - <i>Mus musculus</i>	1872	1245/1874 (66%)	1478/1874 (78%)	0.0
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The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 12D. In the ClustalW alignment of the NOV12 protein, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.

Table 12D. ClustalW Analysis of NOV12

- 1) NOV12 (SEQ ID NO:32)
2) ptnr: PLEXIN 1 - *Mus musculus* (SEQ ID NO:81)
3) ptnr: NOV/PLEXIN-A1 PROTEIN - *Homo sapiens* (SEQ ID NO:82)
4) ptnr: PLEXIN PRECURSOR - *Xenopus laevis* (SEQ ID NO:83)
5) ptnr: Plexin A3 precursor (Plexin 4) (SEQ ID NO:84)
6)

20	NOV12 P70206 Q9UW2 Q91823 PS1805	MMLTPAGPHERGPRQPAMP-----PPRSILQLLLLLLILLPCVNAABSLPRAACGSCOPPFRTFSASDWGLTHLVHVBOTEG -----PLPLLSRTLLLILLLLIPLPISSSPACIGDOPAFTPRTFVAWSGLWLTHLVHVBOTEG -----DIAAEALPRAACGSCOPPFRTFEGDSWGLWLTHLVHVBOTEG -----LLHAERPLPPHTMPLFLVILGSPTPT-----GIGSPKIFRTFGSDMSTLTHLVHVBOTEG -----PSVCLLULLFPLAV-----GALGNRPFAFVVDLTLTHLVHVBOTEG	44
25	NOV12 P70206 Q9UW2 Q91823 PS1805	VYVGAVNRYIKLSCMLTLLRAHVTGPVEDNEKCYPPPSVQSCPMLGCSIDAWYKLLELDYANARLLACCGSASOGICOFPL VYVGAVNRYIKLSCMLTLLRAHVTGPVEDNEKCYPPPSVQSCPMLGCSIDAWYKLLELDYANARLLACCGSASOGICOFPL VYVGAVNRYIKLSCMLTLLRAHVTGPVEDNEKCYPPPSVQSCPMLGCSIDAWYKLLELDYANARLLACCGSASOGICOFPL VYVGAVNRYIKLSCMLTLLRAHVTGPVEDNEKCYPPPSVQSCPMLGCSIDAWYKLLELDYANARLLACCGSASOGICOFPL VYVGAVNRYIKLSCMLTLLRAHVTGPVEDNEKCYPPPSVQSCPMLGCSIDAWYKLLELDYANARLLACCGSASOGICOFPL	160 140 120 135 124
30	NOV12 P70206 Q9UW2 Q91823 PS1805	LDDLFKLCPGEHRRKEHYLSSVEAGSMAGVLIAACPPGCGOAKLFLVGTIPDGKSEYFPTRSSRLMLNEEDADMFGFYVOE LDDLFKLCPGEHRRKEHYLSSVEAGSMAGVLIAACPPGCGOAKLFLVGTIPDGKSEYFPTRSSRLMLNEEDADMFGFYVOE LDDLFKLCPGEHRRKEHYLSSVEAGSMAGVLIAACPPGCGOAKLFLVGTIPDGKSEYFPTRSSRLMLNEEDADMFGFYVOE LDDLFKLCPGEHRRKEHYLSSVEAGSMAGVLIAACPPGCGOAKLFLVGTIPDGKSEYFPTRSSRLMLNEEDADMFGFYVOE LDDLFKLCPGEHRRKEHYLSSVEAGSMAGVLIAACPPGCGOAKLFLVGTIPDGKSEYFPTRSSRLMLNEEDADMFGFYVOE	240 220 200 160 202
35	NOV12 P70206 Q9UW2 Q91823 PS1805	EFVSSLQ1PSDTLSKFPAFDIYVVYFSRSEQFVYLTQDOLTLSPDAAEHFTSKIVRLCVWDPKFYSVVFPIG EFVSSLQ1PSDTLSKFPAFDIYVVYFSRSEQFVYLTQDOLTLSPDAAEHFTSKIVRLCVWDPKFYSVVFPIG EFVSSLQ1PSDTLSKFPAFDIYVVYFSRSEQFVYLTQDOLTLSPDAAEHFTSKIVRLCVWDPKFYSVVFPIG EFVSSLQ1PSDTLSKFPAFDIYVVYFSRSEQFVYLTQDOLTLSPDAAEHFTSKIVRLCVWDPKFYSVVFPIG	320 300 280 160 282
40	NOV12 P70206 Q9UW2 Q91823 PS1805	EOAGVEYRLVQDAYLSRPGCALAHOLGLAEDBVLFVFAOGOGRVVKPPKESALCLFTLRAIKEKIKERIOSCYRGEG EOAGVEYRLVQDAYLSRPGCALAHOLGLAEDBVLFVFAOGOGRVVKPPKESALCLFTLRAIKEKIKERIOSCYRGEG EOAGVEYRLVQDAYLSRPGCALAHOLGLAEDBVLFVFAOGOGRVVKPPKESALCLFTLRAIKEKIKERIOSCYRGEG SWRGEVEYRLVQDAYLSRPGCALAHOLGLAEDBVLFVFAOGOGRVVKPPKESALCLFTLRAIKEKIKERIOSCYRGEG	400 380 360 160 362
45	NOV12 P70206 Q9UW2 Q91823 PS1805	LSLPWLLNKELGCIISPLQIUDDFCGQDNOPLCGTVTIECTPLFLVNDGLTAVAAYDYRGRTVVFACTRSQRKILV LSLPWLLNKELGCIISPLQIUDDFCGQDNOPLCGTVTIECTPLFLVNDGLTAVAAYDYRGRTVVFACTRSQRKILV LSLPWLLNKELGCIISPLQIUDDFCGQDNOPLCGTVTIECTPLFLVNDGLTAVAAYDYRGRTVVFACTRSQRKILV JALPWLLNKELGCIISPLQIUDDFCGQDNOPLCGTVTIECTPLFLVNDGLTAVAAYDYRGRTVVFACTRSQRKILV	480 460 440 160 442
50	NOV12 P70206 Q9UW2 Q91823 PS1805	DLSNIGRPLALYESVVAOEGLPILRDLVLSIHNHOYLAXTEKOVITVPVPECSVCVYTSCEFLCLGSRDPHCCWCVLHSIS DLSNIGRPLALYESVVAOEGLPILRDLVLSIHNHOYLAXTEKOVITVPVPECSVCVYTSCEFLCLGSRDPHCCWCVLHSIS DLSNIGRPLALYESVVAOEGLPILRDLVLSIHNHOYLAXTEKOVITVPVPECSVCVYTSCEFLCLGSRDPHCCWCVLHSIS GG-----FDDPHLYEAVPVVEGSPILRDLVNSP-----LSEKVSQLPVEIOPDVSACCLGSRDPHCCWCVLHSIS	560 540 520 160 518
55	NOV12 P70206 Q9UW2 Q91823 PS1805	FNDACERADEPORFADLLCQCVOILTVOFFVSVTMSQVFVVLQOANNVPDLSAGWICSFEDFTESVSILE-DGR1HCRSF FNDACERADEPORFADLLCQCVOILTVOFFVSVTMSQVFVVLQOANNVPDLSAGWICSFEDFTESVSILE-DGR1HCRSF FNDACERADEPORFADLLCQCVOILTVOFFVSVTMSQVFVVLQOANNVPDLSAGWICSFEDFTESVSILE-DGR1HCRSF REGAALGCSAHCFAEBSKCVDRVRIINNSVTSPLCQ-1ITLTHNNVPDLSAGWICSFEDFTESVSILE-DGR1HCRSF	639 618 598 160 597
60	NOV12 P70206 Q9UW2 Q91823 PS1805	SAREVAPITRCGCCGDQRVVNLYLKSKEGKFKASFVDFVFVNCVSQHOSCLSCVNGSPCHWCKYRHCVTHNADCAFLE SAREVAPITRCGCCGDQRVVNLYLKSKEGKFKASFVDFVFVNCVSQHOSCLSCVNGSPCHWCKYRHCVTHNADCAFLE	719 695
65	NOV12 P70206		

5	Q9UIW2 Q91823 P51805	SAREVAPITRGK - GDOVRVVKLPIKSKSETOKKFAVDFVFVNCVHS - CLSCVNGSPFCHWCKYRHCVMMADCAFE SLGFRATRCH - CATFVRLQIISKGTVFRAQADFVFVNCVLS - CXCSCOSPVCHWCKYRHICSRPHCSPE	674
10	NOV12 P70206 Q9UIW2 Q91823 P51805	GRVMSEDCPOILPSTCIVYPVGVKPITLAAPNIPOPOSCORGVECLFHIPGSPARVTALRFNSSSLOCNNSSYECN GRVMSEDCPOILPSTCIVYPVGVKPITLAAPNLPOPOSCORGVECLFHIPGSPARVTALRFNSSSLOCNNSSYECN GRVMSEDCPOILPSTCIVYPVGVKPITLAAPLPOPOSCORGVECLFHIPGSPARVTALRFNSSSLOCNNSSYECN	799 775 755
15	NOV12 P70206 Q9UIW2 Q91823 P51805	DVSDLPVNLSSVVMCFIVDNPONIOAHLYKCPALPSCGLCLRADPRFCFGCWVAERRCSLRHICADPASHWHARIG DVSDLPVNLSSVVMCFIVDNPONIOAHLYKCPALPSCGLCLRADPRFCFGCWVAERRCSLRHICADPASHWHARIG DVSDLPVNLSSVVMCFIVDNPONIOAHLYKCPALPSCGLCLRADPRFCFGCWVAERRCSLRHICADPASHWHARIG	879 855 835
20	NOV12 P70206 Q9UIW2 Q91823 P51805	HCETEYDFSVVADCDPHELKNTPSFRALLYKCPALPSCGLCLRADPRFCFGCWICISPRRCOIFMCPAKPTNMHLSQK SSRCTDPKILKLSPETCPROGCTRLTTCGMLGLRFEVRLGVWGVKLCSPVSEYIASAEQIVCEICDASSVRAHALDV SSRCTDPKILKLSPETCPROGCTRLTTCGMLGLRFEVRLGVWGVKLCSPVSEYIASAEQIVCEICDASSVRAHALDV	959 935 915
25	NOV12 P70206 Q9UIW2 Q91823 P51805	SSRCTDPKILKLSPETCPROGCTRLTTCGMLGLRFEVRLGVWGVKLCSPVSEYIASAEQIVCEICDASSVRAHALDV SSRCTDPKILKLSPETCPROGCTRLTTCGMLGLRFEVRLGVWGVKLCSPVSEYIASAEQIVCEICDASSVRAHALDV SSRCTDPKILKLSPETCPROGCTRLTTCGMLGLRFEVRLGVWGVKLCSPVSEYIASAEQIVCEICDASSVRAHALDV	160 911
30	NOV12 P70206 Q9UIW2 Q91823 P51805	EVCVRDCS ^{HYRALSPKRFTFVTPFYRVSPSRGPSSGGTWIGIEGSHAGSCAVAVSGRCPCSFSKSPNSREIRCL1} EVCVRDCS ^{HYRALSPKRFTFVTPFYRVSPSRGPSSGGTWIGIEGSHAGSCAVAVSGRCPCSFSKSPNSREIRCL1} EVCVRDCS ^{HYRALSPKRFTFVTPFYRVSPSRGPSSGGTWIGIEGSHAGSCAVAVSGRCPCSFSKSPNSREIRCL1} EVCVRDCS ^{HYRALSPKRFTFVTPFYRVSPSRGPSSGGTWIGIEGSHAGSCAVAVSGRCPCSFSKSPNSREIRCL1}	1039 1013 993 989
35	NOV12 P70206 Q9UIW2 Q91823 P51805	PPCGP ^{PGSAPITIINRQAOLIPEVKYNTTEDPTILRIDPEWSINSGGTLTTVTCGMLATVREPRIRAKYGGIEREN-C} PPGHP ^{PGSAPITIINRQAOLIPEVKYNTTEDPTILRIDPEWSINSGGTLTTVTCGMLATVREPRIRAKYGGIEREN-C} PPCGP ^{PGSAPITIINRQAOLIPEVKYNTTEDPTILRIDPEWSINSGGTLTTVTCGMLATVREPRIRAKYGGIEREN-C} PLSTLCPSGAPITIANDAMIESPCG ^{IITNTCDPDXRASTASITGSIAUTVSGDILITVQEPFIRAKYGGIBITMC}	1117 1092 1072 1069
40	NOV12 P70206 Q9UIW2 Q91823 P51805	WYNDITTMVCRAPS ^{VANFRSPPELGERPDEI} WYNDITTMVCRAPS ^{VANFRSPPELGERPDEI} WYNDITTMVCRAPS ^{VANFRSPPELGERPDEI} QINDIANA ^{QACPLQRPOBRAQCBPDRFICPLIUVXARSINRESITYPDHSFEPICPSGVDAKPSHIVLKGK}	1197 1172 1152 1149
45	NOV12 P70206 Q9UIW2 Q91823 P51805	NLLPPAPCNSRNYTVLIGSTPC ^{LTVSETOLLCEAPNLTGQHKVTVRAGGFEPSPGTLOVYSDSLLTLPATVGI} NLLPPAPCNSRNYTVLIGSTPC ^{LTVSETOLLCEAPNLTGQHKVTVRAGGFEPSPGTLOVYSDSLLTLPATVGI} NLLPPAPCNSRNYTVLIGSTPC ^{LTVSETOLLCEAPNLTGQHKVTVRAGGFEPSPGTLOVYSDSLLTLPATVGI} NUIPAAESRNRNYTVLIGSTPC ^{LTVSETOLLCEAPNLTGQHKVTVRAGGFEPSPGTLOVYSDSLLTLPATVGI}	1277 1252 1232 1229
50	NOV12 P70206 Q9UIW2 Q91823 P51805	LLLLVIVAVLIAYKRKSRADRTLKLRLQLQMDLESRVALECKEAFALQTDIHELTNDLDGAGIPFLDYRTYMRVLFF LLLLVIVAVLIAYKRKSRADRTLKLRLQLQMDLESRVALECKEAFALQTDIHELTNDLDGAGIPFLDYRTYMRVLFF LLLLVIVAVLIAYKRKSRADRTLKLRLQLQMDLESRVALECKEAFALQTDIHELTNDLDGAGIPFLDYRTYMRVLFF LLLLVIVAVLIAYKRKSRADRTLKLRLQLQMDLESRVALECKEAFALQTDIHELTNDLDGAGIPFLDYRTYMRVLFF	1357 1332 1312 1309
55	NOV12 P70206 Q9UIW2 Q91823 P51805	GIEDHPVLMEMEVQANVEKS ^{LTFQCOLLTKHHFLLTIRTLEAQRSFSMRDRQVASLIMTALOGEMEYATGVLKOLLSC} GIEDHPVLMEMEVQANVEKS ^{LTFQCOLLTKHHFLLTIRTLEAQRSFSMRDRQVASLIMTALOGEMEYATGVLKOLLSC} GIEDHPVLMEMEVQANVEKS ^{LTFQCOLLTKHHFLLTIRTLEAQRSFSMRDRQVASLIMTALOGEMEYATGVLKOLLSC} CLEANHVKLEM ^{PTPENVERAHLTFQCOLLTKHHFLLTIRTLEAQRSFSMRDRQVASLIMTALOGEMEYATGVLKOLLSC}	1437 1412 1392 1389
60	NOV12 P70206 Q9UIW2 Q91823 P51805	LIENMLESNNHPKLLRR ^{-TESVAEMLNWFTEFLYKFIKECAGPFLMLYCAIKCQMEKGPDIAITGEARYSLEDKL} LIENMLESNNHPKLLRR ^{-TESVAEMLNWFTEFLYKFIKECAGPFLMLYCAIKCQMEKGPDIAITGEARYSLEDKL} LIENMLESNNHPKLLRR ^{-TESVAEMLNWFTEFLYKFIKECAGPFLMLYCAIKCQMEKGPDIAITGEARYSLEDKL} LIENMLESNNHPKLLRR ^{-TESVAEMLNWFTEFLYKFIKECAGPFLMLYCAIKCQMEKGPDIAITGEARYSLEDKL}	1517 1491 1471 1468
65	NOV12 P70206 Q9UIW2 Q91823 P51805	IROQIDYKLTLCV ^{PEVAPVPKLGCLDFTVTOAKEKLLDPAKGVPSQRPKAMDLEWRQGRMARIILODEDV} IROQIDYKLTLCV ^{PEVAPVPKLGCLDFTVTOAKEKLLDPAKGVPSQRPKAMDLEWRQGRMARIILODEDV} IROQIDYKLTLCV ^{PEVAPVPKLGCLDFTVTOAKEKLLDPAKGVPSQRPKAMDLEWRQGRMARIILODEDV} IROQIDYKLTLCV ^{PEVAPVPKLGCLDFTVTOAKEKLLDPAKGVPSQRPKAMDLEWRQGRMARIILODEDV}	1597 1571 1551 160
70	NOV12 P70206 Q9UIW2 Q91823 P51805	ITKIDNDWKRL ^{PLAHYQVTDGSSVALVPKOTSAYNIS} ITKIDNDWKRL ^{PLAHYQVTDGSSVALVPKOTSAYNIS} ITKIDNDWKRL ^{PLAHYQVTDGSSVALVPKOTSAYNIS} ITKIDNDWKRL ^{PLAHYQVTDGSSVALVPKOTSAYNIS}	1677 1651 1631 160
75	NOV12 P70206 Q9UIW2 Q91823 P51805	ITKIDNDWKRL ^{PLAHYQVTDGSSVALVPKOTSAYNIS} ITKIDNDWKRL ^{PLAHYQVTDGSSVALVPKOTSAYNIS} ITKIDNDWKRL ^{PLAHYQVTDGSSVALVPKOTSAYNIS} ITKIDNDWKRL ^{PLAHYQVTDGSSVALVPKOTSAYNIS}	1677 1651 1631 160
80	NOV12 P70206 Q9UIW2 Q91823 P51805	WHILVNNHDHLDQREGDRGSKM ^{SEIYLTRLATKC} WHILVNNHDHLDQREGDRGSKM ^{SEIYLTRLATKC} WHILVNNHDHLDQREGDRGSKM ^{SEIYLTRLATKC} WHILVNNHDHLDQREGDRGSKM ^{SEIYLTRLATKC}	1757 1730 1710 160
85	NOV12 P70206 Q9UIW2 Q91823 P51805	DGDVRHTWKSNC ^{-PFLQFVDDLFETIFSTAHRGSALPLAIKYMFDLDEQADKHOI} DGDVRHTWKSNC ^{-PFLQFVDDLFETIFSTAHRGSALPLAIKYMFDLDEQADKHOI} DGDVRHTWKSNC ^{-PFLQFVDDLFETIFSTAHRGSALPLAIKYMFDLDEQADKHOI} DGDVRHTWKSNC ^{-PFLQFVDDLFETIFSTAHRGSALPLAIKYMFDLDEQADKHOI}	1837 1809 1754 1704
90	NOV12 P70206 Q9UIW2 Q91823 P51805	WVEPYDIANRPAISDODRS ^{TYLAEOSRRLHSCENS} WVEPYDIANRPAISDODRS ^{TYLAEOSRRLHSCENS}	1917 1886

Q9UIW2 ----- 1754
Q91823 ----- 160
P51805 ~~NVES WYNDIARYA~~ LSDQDN DAYI MEGSRILASDFSV ~~ISALNLSWTFYRSDO - EII RUPRABASEXHUFONIEQ~~ 1863

NOV12 ~~JDTMALS~~ 1925
P70206 ~~JDTMALS~~ 1894
Q9UIW2 ----- 1754
Q91823 ----- 160
P51805 ~~MSLVYSD~~ 1871

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Tables 12E-12N list the domain descriptions from DOMAIN analysis results against NOV12. This indicates that the NOV12 sequence has properties similar to those of other proteins known to contain this domain.

Table 12E. Domain Analysis of NOV12

gnl|Smart|smart00630, Sema, semaphorin domain (SEQ ID NO:113)
CD-Length = 430 residues, 100.0% aligned
Score = 242 bits (618), Expect = 1e-64

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